GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:46:53 ; Search time 176 Seconds
(without alignments)
5169.360 Million cell updates/sec

Title: US-09-975-842-1
Perfect score: 404
Sequence: 1 gggttgccggggttcaggat.....cccggctactttagcctctg 404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		194.8	48.2	1743	19	AAV30330	Rose 1-aminocyclop
c 2		107.6	26.6	748	24	ABQ65439	Arabidopsis thalia
3		98	24.3	1384	17	AAT33136	Broccoli ACC synth
4		93.2	23.1	3438	20	AAX35671	DNA encoding a 1-a
5		86.6	21.4	961	19	AAV00220	1-aminocyclopropan
6		84.6	20.9	968	19	AAV00219	1-aminocyclopropan
7		83.6	20.7	1170	18	AAT66247	ACC synthase GAC-2
8		83.6	20.7	1878	19	AAV30326	Pelargonium 1-amin
9		82.2	20.3	993	17	AAT33139	Broccoli ACC synth
10		82	20.3	1868	18	AAT73502	Poplar 1-aminocycl
11		80.8	20.0	1864	18	AAT73501	Poplar 1-aminocycl
12		80.4	19.9	1096	18	AAT72631	Mangifera indica A
13		80.4	19.9	1113	18	AAT72632	Mangifera indica A
14		78.8	19.5	1712	20	AAX27501	Banana 1-aminocycl
15		78.8	19.5	1712	22	AAS09901	DNA encoding 1-ami
16		77	19.1	1080	18	AAT72628	Ananas comosus ACC
17		72.4	17.9	1087	17	AAT38897	Carnation ACC synt
18		72.4	17.9	1942	17	AAT38896	Carnation ACC synt
19		72.4	17.9	1945	19	AAV30324	Pelargonium 1-amin
20		72.4	17.9	2088	19	AAV20947	Coffee-fruit speci
21		72.4	17.9	2678	19	AAV30325	Pelargonium 1-amin
22		69.2	17.1	1482	13	AAQ25896	ACC synthetase gen
23		69.2	17.1	1934	18	AAT66246	ACC synthase GAC-1
24		67.6	16.7	1703	12	AAQ15131	Clone pACC1 encodi
25		67.6	16.7	1703	19	AAV15701	Zucchini ACC synth
26		67.6	16.7	1703	22	AAD04541	Zucchini 1-aminocy
27		67.6	16.7	1703	22	AAF23618	Zucchini ACC synth
28		67.6	16.7	1923	21	AAZ94267	Mung bean ACC synt
29		65	16.1	7241	12	AAQ15140	Genomic clone LE-A
30		64.4	15.9	1104	18	AAT72629	Carica papaya ACC
31		64.4	15.9	1775	12	AAQ15134	Clone ptACC1 encod
32		64.4	15.9	1818	22	AAD04546	Tomato 1-aminocycl
33		64.4	15.9	2230	19	AAV15704	Tomato ACC synthas
34		64.4	15.9	2230	22	AAD04544	Tomato 1-aminocycl
35		64.4	15.9	2230	22	AAF23621	Tomato ACC synthas
36		64.4	15.9	7244	19	AAV15705	Tomato ACC synthas
37		64.4	15.9	7244	22	AAD04545	Tomato 1-aminocycl
38		64.4	15.9	7244	22	AAF23622	Tomato ACC synthas
39		63.2	15.6	5613	15	AAQ63241	Crucifer 1-aminocy
40		62.8	15.5	15397	18	AAT58635	T-DNA insert of 13
c 41		62.8	15.5	15397	18	AAT58635	T-DNA insert of 13
42		61.2	15.1	1800	19	AAV09713	ACC synthase DNA.
43		59.6	14.8	1888	19	AAV31482	Papaya ACC synthas
44		58.4	14.5	1098	18	AAT72630	Carica papaya ACC
45		48.2	11.9	7587	12	AAQ15133	Zucchini ACC synth

ALIGNMENTS

RESULT 1
AAV30330
ID AAV30330 standard; cDNA; 1743 BP.
XX
AC AAV30330;
XX
DT 28-SEP-1998 (first entry)
XX
DE Rose 1-aminocyclopropane-1-carboxylase synthase cDNA pRoseKacc7.
XX
KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
KW ethylene; transgenic plant; wilting; rose; pRoseKacc7; ss.
XX
OS Rosa sp. cv. Cardinal Red.
XX
FH Key Location/Qualifiers
FT CDS 271..1713
FT /*tag= a
FT misc_feature complement (1..50)
FT /*tag= c
FT /note= "antisense oligonucleotide (Claim 18)"
FT misc_feature complement (51..100)
FT /*tag= d
FT /note= "antisense oligonucleotide (Claim 18)"
FT misc_feature complement (101..150)
FT /*tag= e
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FT misc_feature complement (151..200)
FT /*tag= f
FT /note= "antisense oligonucleotide (Claim 18)"
FT misc_feature complement (201..250)
FT /*tag= g

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FT   misc_feature    complement (251..300)
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FT   misc_feature    complement (351..400)
FT                   /*tag= j
FT                   /note= "antisense oligonucleotide (Claim 18)"
FT   misc_feature    complement (401..450)
FT                   /*tag= k
FT                   /note= "antisense oligonucleotide (Claim 18)"
FT   misc_feature    complement (451..500)
FT                   /*tag= l
FT                   /note= "antisense oligonucleotide (Claim 18)"
FT   misc_feature    complement (1..1945)
FT                   /*tag= m
FT                   /note= "any contiguous 50 nucleotides (Claim 18)"
XX
PN   WO9814465-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17644.
XX
PR   01-OCT-1996;   96US-0724194.
XX
PA   (COLS ) UNIV COLORADO STATE RES FOUND.
XX
PI   Ranu RS;
XX
DR   WPI; 1998-260994/23.
DR   P-PSDB; AAW60239.
XX
PT   New isolated ACC synthase genes - are obtained from geranium and
PT   rose, used to develop products for producing plants with reduced
PT   ethylene levels, for increasing shelf-life
XX
PS   Claim 6; Fig 9; 77pp; English.
XX
CC   This cDNA clone, designated pRoseKacc7, codes for a
CC   1-aminocyclopropane-1-carboxylate synthase (ACC synthase) (see
CC   AAW60239) of rose (cv. Red Cardinal).  High quality mRNA was obtained
CC   from flower tissue using a novel adaptation of the 2-butoxyethanol
CC   precipitation technique.  This was converted to cDNA and screened
CC   with a probe generated by PCR amplification (see AAV30328-29).  The
CC   pRoseKacc7 clone was obtained.  3 Geranium ACC synthase clones (see
CC   AAV30324-26) are also claimed.  The ACC synthase genes, or their
CC   fragments, when introduced in antisense orientation under control
CC   of a strong promoter, can be used to genetically modify a plant,
CC   especially geranium, rose or woody plant.  As a consequence, the
CC   amount of ACC synthase produced in the plant cells is reduced and
CC   the rate of ACC conversion to ethylene decreases.  This can be used
CC   to prolong the shelf-life of cut flowers and to reduce leaf
CC   yellowing and petal abscission during shipping and storage.
XX
SQ   Sequence 1743 BP; 429 A; 401 C; 442 G; 471 T; 0 other;

  Query Match             48.2%;  Score 194.8;  DB 19;  Length 1743;
  Best Local Similarity   71.2%;  Pred. No. 9.8e-58;
  Matches  285;  Conservative    0;  Mismatches  112;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
Db    1232 TTCCAGGTTTCAGGGTGGGTGCCATCTACTCCTTTAACAAGAATGTCTTGACTGCTGCTA 1291

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
Db    1292 AAAAGTTGACAAGGTTCTCTTCTATCTCCGCCCCATCCCAACGGTTGCTTATCTCTATGC 1351

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
Db    1352 TTTCAGACACCAAATTTATGCATAAGTTCATCGAGATTAACAGAGAAAGGCTCCGTGGAA 1411

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
Db    1412 TGTATCTTAGATTTGTGAC-AGGATTGAAGCAATTGGGCATTGAGTGCACAAAGAGCAAT 1470

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
Db    1471 GGGGG--TTTCTACTGTTGGGCAGACTTGAGTGGGTTAATTCGCTCTTACAGTGAGAAAG 1528

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
Db    1529 GGGAGCTTGAGCTCTGGGATAGGTTGTTGAATGTAGGTAAGCTCAATGTTACTCCTGGAT 1588

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1589 CTTCTTGTCATTGTATTGAACCGGGATGGTTCCGGTTTTG 1628


RESULT 2
ABQ65439/c
ID   ABQ65439 standard; DNA; 748 BP.
XX
AC   ABQ65439;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Arabidopsis thaliana polynucleotide SEQ ID NO 16.
XX
KW   Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
KW   stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
KW   insecticide; antibiotic; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   US2002059663-A1.
XX
PD   16-MAY-2002.
XX
PF   26-JAN-2001; 2001US-0770149.
XX
PR   27-JAN-2000; 2000US-178506P.
XX
PA   (GORL/) GORLACH J.
PA   (ANYY/) AN Y.
PA   (HAMI/) HAMILTON C M.
PA   (PRIC/) PRICE J L.
PA   (RAIN/) RAINES T M.
PA   (YUYY/) YU Y.
PA   (RAME/) RAMEAKA J G.
PA   (PAGE/) PAGE A.
PA   (MATH/) MATHEW A V.
PA   (LEDF/) LEDFORD B L.
PA   (WOES/) WOESSNER J P.
PA   (HAAS/) HAAS W D.
PA   (GARC/) GARCIA C A.
PA   (KRIC/) KRICKER M.
PA   (SLAT/) SLATER T.
PA   (DAVI/) DAVIS K R.
PA   (ALLE/) ALLEN K.
PA   (HOFF/) HOFFMAN N.
PA   (HURB/) HURBAN P.
XX
PI   Gorlach J,  An Y,  Hamilton CM,  Price JL,  Raines TM,  Yu Y;
PI   Rameaka JG,  Page A,  Mathew AV,  Ledford BL,  Woessner JP,  Haas WD;
PI   Garcia CA,  Kricker M,  Slater T,  Davis KR,  Allen K,  Hoffman N;
PI   Hurban P;
XX
DR   WPI; 2002-479224/51.
XX
PT   New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
PT   useful e.g. for preparing transgenic plants with increased resistance
PT   or altered metabolism -
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XX
PS   Claim 1; SEQ ID NO 16; 40pp + Sequence Listing; English.
XX
CC   The invention relates to nucleic acids (I) that hybridise under stringent
CC   conditions to any of 999 sequences (ABQ65424-ABQ66422) or their
CC   fragments. (I) are used to express the corresponding polypeptides (II) or
CC   to produce genetically modified plant cells or transgenic plants, which
CC   may have improved resistance to disease or stress, or altered
CC   metabolic/biosynthetic pathways (for production of commercial,
CC   nutritional or medicinal products), or generally any trait of interest,
CC   or can be used to screen for biologically active agents (e.g. fungicides,
CC   insecticides and antibiotics).
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149.
XX
SQ   Sequence 748 BP; 209 A; 202 C; 120 G; 213 T; 4 other;

  Query Match             26.6%;  Score 107.6;  DB 24;  Length 748;
  Best Local Similarity   57.4%;  Pred. No. 3.2e-27;
  Matches  232;  Conservative    0;  Mismatches  169;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     617 GGTCTTCCTGGTTTCCGCGTGGGAACTATATACTCGTACAACGATAATGTTGTTCGGACA 558

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     557 GCGAGAAGGATGTCGAGCTTCACGCTTGTCTCGTCTCAGACACAACATATGCTGGCTTCT 498

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     497 ATGTTGTCGGATGAGGAGTTTACGGAGAAGTACATTAGGATAAACCGGGAAAGACTTAGA 438

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     437 AGACGGTACGATACCATTGTGGAAGGGCTT-AAGAAGGCAGGGATTGAGTGTTTGAAAGG 379

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     378 GAACGCAGG--GCTATTTTGTTGGATGAATTTGGGTTTCTTGCTCGAAAAGAAAACTAAA 321

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     320 GACGGCGAGCTCCAGCTTTGGGATGTGATCTTAAAGGAGCTGAACCTGAATATATCTCCG 261

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db     260 GGATCTTCGTGCCACTGCTCGGAGGTCGGATGGTTTAGGGTTTG 217

.
RESULT 3
AAT33136
ID   AAT33136 standard; DNA; 1384 BP.
XX
AC   AAT33136;
XX
DT   07-DEC-1996  (first entry)
XX
DE   Broccoli ACC synthase genomic DNA clone ACCA1.
XX
KW   ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;
KW   ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
KW   antisense; broccoli; ss.
XX
OS   Brassica oleracea.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (1..31)
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FT                   /note= "primer RMM393"
FT   exon            1..37
FT                   /*tag=  b
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FT   intron          38..134
FT                   /*tag=  c
FT   exon            135..431
FT                   /*tag=  d
FT   intron          432..594
FT                   /*tag=  e
FT   exon            595..1384
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FT   primer_bind     1352..1382
FT                   /*tag=  g
FT                   /note= "primer RMM394"
XX
PN   WO9621027-A1.
XX
PD   11-JUL-1996.
XX
PF   07-JUN-1995;   95WO-US07271.
XX
PR   30-DEC-1994;   94US-0366992.
XX
PA   (ASGR-) ASGROW SEED CO.
XX
PI   Boeshore ML,  Carney KJ,  Deng RZ,  Reynolds JF,  Ruttencutter GE;
XX
DR   WPI; 1996-334002/33.
DR   P-PSDB; AAR98598.
XX
PT   DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of
PT   Brassica oleracea - used to regulate ethylene-dependent processes
PT   in plants, esp. to improve shelf life
XX
PS   Claim 2; Fig1A-B; 50pp; English.
XX
CC   Brassica oleracea genomic clone ACCA1 (AAT33136) codes for
CC   1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
CC   (AAR98598), an enzyme involved in ethylene biosynthesis.  It was
CC   obtd. by subjecting broccoli leaf total genomic DNA to PCR using
CC   primers (see also AAT33137-38) based on the Arabidopsis thaliana ACC
CC   synthase gene.  The product was cloned into pCRII to obtain clone
CC   ACCA1.  Genomic DNA or cDNA (see also AAT33139) can be inserted, in
CC   sense or antisense orientation, into an expression cassette and then
CC   transferred to a binary vector suitable for Agrobacterium-mediated
CC   plant transformation.  The constructs permit control of the level of
CC   ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
CC   melo) and hence a control of maturation, ageing and shelf-life.
XX
SQ   Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T; 0 other;

  Query Match             24.3%;  Score 98;  DB 17;  Length 1384;
  Best Local Similarity   55.9%;  Pred. No. 1.1e-23;
  Matches  226;  Conservative    0;  Mismatches  175;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     970 GGTCTTCCCGGTTTTCGAGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA 1029

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db    1030 GCGAGAAGGATGTCGAGTTTCACGCTTGTCTCGTCTCAGACACAACACATGTTGGCTTCC 1089

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db    1090 ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 1149

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db    1150 AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG 1208

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db    1209 TAATGCAGGGT--TGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA 1266
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Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |||| |||||||||||| |||||    | |  | ||       ||| | ||  |  ||||
Db    1267 CAAGGCGAGCTCGAGCTTTGGGATGTGATCTTGAAGGAACTAAAGCTGAATATATCTCCT 1326

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || ||||  || |||||    ||    || |  |||||  | ||
Db    1327 GGATCTTCGTGCCATTGCTCGGAGTATGGATGGTTTAGGATTTG 1370


RESULT 4
AAX35671
ID   AAX35671 standard; DNA; 3438 BP.
XX
AC   AAX35671;
XX
DT   16-JUL-1999  (first entry)
XX
DE   DNA encoding a 1-aminocyclopropane-1-carboxylic acid oxidase.
XX
KW   Localised mutation; target gene; plant cell;
KW   recombinogenic oligonucleobase; selective growth advantage;
KW   herbicide resistance; preservation; fruit; flower; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   WO9907865-A1.
XX
PD   18-FEB-1999.
XX
PF   05-AUG-1998;   98WO-US16267.
XX
PR   05-AUG-1997;   97US-0054836.
XX
PA   (KIME-) KIMERAGEN INC.
XX
PI   Arntzen CJ,  Kipp PB,  Kumar R,  May GD;
XX
DR   WPI; 1999-302251/25.
XX
PT   Introducing mutations into target genes in plant cells - using a
PT   recombinogenic oligonucleobase comprising 2 regions homologous to a
PT   target gene and an intervening mutant region
XX
PS   Example 7; Page 46-47; 53pp; English.
XX
CC   The specification describes methods for introducing localized mutations
CC   into target genes in plant cells. The methods comprise using a
CC   recombinogenic oligonucleobase comprising 2 regions homologous to a
CC   target gene and an intervening mutant region. The methods can be used
CC   to introduce localized mutations into target genes to introduce desirable
CC   traits, e.g. selective growth advantage under appropriate selective
CC   conditions, change in colour of plant cells growing in a callus,
CC   herbicide resistance, or improved preservation of fruit or flowers.
CC   They can be used in plants such as maize, wheat, rice, lettuce, potato,
CC   tomato, canola, soybean or cotton cell. The present sequenc represents
CC   a target for the methods of the invention.
XX
SQ   Sequence 3438 BP; 1084 A; 647 C; 599 G; 1108 T; 0 other;

  Query Match             23.1%;  Score 93.2;  DB 20;  Length 3438;
  Best Local Similarity   55.2%;  Pred. No. 8.3e-22;
  Matches  223;  Conservative    0;  Mismatches  178;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || || ||  | || |  || |||||| |  || |  | ||  || || |
Db    2294 GGCCTCCCTGGTTTTAGAGTTGGAGCCATTTACTCCAATGACAAAGATGTCATCTCTGCC 2353

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || | |||  || | || ||        | ||  | | ||| ||   | | ||   |
Db    2354 GCTACAAAAATGTCAAGTTTCGGCCTTGTCTCCTCCCAGACACAATACCTACTATCCTCA 2413

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           |  | || |||| |  |||||||  | || | | |    |  |||  |      |||||

Db    2414 TTATTATCTGACAAGAAGTTCACTAAGAACTACCTTAGAGAGAACCAAAAACGGCTCAAG 2473

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           |  |   |        |||||  |||  | || |  | |||| |||  |||   | | ||
Db    2474 AACAGACAGAGAAAGCTCGTGTTGGGTCTAGAGGCCA-TCGGGATCAAATGTCTGAAGAG 2532

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           |  |  ||   |||| |||||||| |||||||||      |  || ||||  | |
Db    2533 TAATGCGGG--ACTCTTTTGTTGGGTCGACATGAGACCTCTCCTTAGATCTAAAACGTTC 2590

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |||  ||  | || || ||| | ||| |  |  ||    |  ||| | ||| |  ||||
Db    2591 GAAGCGGAAATGGATCTTTGGAAGAAGATTGTTTACGAAGTGAAGCTCAACATCTCTCCT 2650

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||||| |  || ||||||   ||||| || |  |||||  | ||
Db    2651 GGTTCGTCGTGCCATTGTGAAGAACCGGGTTGGTTTAGAGTTTG 2694


RESULT 5
AAV00220
ID   AAV00220 standard; DNA; 961 BP.
XX
AC   AAV00220;
XX
DT   08-JUN-1998  (first entry)
XX
DE   1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.
XX
KW   1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
KW   flowering; inhibition; regulation; development; fruit; ss.
XX
OS   Ananas comosus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..961
FT                   /*tag=  a
FT                   /product= "acacc3"
FT                   /note= "no stop codon given; contains an intron"
FT   exon            1..101
FT                   /*tag=  b
FT                   /number= 1
FT   intron          102..193
FT                   /*tag=  c
FT                   /number= 1
FT   exon            194..961
FT                   /*tag=  d
FT                   /number= 2
XX
PN   AU9719963-A.
XX
PD   06-NOV-1997.
XX
PF   01-MAY-1997;   97AU-0019963.
XX
PR   01-MAY-1996;   96AU-0009582.
XX
PA   (GOLD-) GOLDEN CIRCLE LTD.
PA   (QUEE-) STATE QUEENSLAND.
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Botella J,  Sanewski G;
XX
DR   WPI; 1998-009279/02.
DR   P-PSDB; AAW37445.
XX
PT   New isolated ACC synthase genes from pineapples - used to generate
PT   transgenic pineapples in which the natural initiation of flowering
PT   is inhibited
XX
PS   Claim 2; Fig 2; 37pp; English.
XX
CC   The present sequence represents the nucleotide sequence encoding a
```

```
CC   1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of
CC   pineapple. The present invention describes a transgenic variety of
CC   pineapple in which initiation of flowering is inhibited, the variety
CC   comprising a nucleotide sequence encoding an ACC synthase enzyme where
CC   the nucleotide sequence is operably linked, in the sense or antisense
CC   orientation, to one or more regulatory nucleotide sequences. The ACC
CC   synthase gene can be used to regulate pineapple plant development,
CC   particularly for inhibiting initiation of flowering. Such plants can
CC   then be induced to flower in a narrow spectrum of time which would
CC   thereby decrease the spread of fruit maturity within a crop.
XX
SQ   Sequence 961 BP; 235 A; 246 C; 247 G; 233 T; 0 other;

  Query Match             21.4%;  Score 86.6;  DB 19;  Length 961;
  Best Local Similarity   55.9%;  Pred. No. 9.2e-20;
  Matches  205;  Conservative    0;  Mismatches  159;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     567 GGGCTACCAGGCTTTCGCGTCGGTGCGATACACTCCCAAAATGAGGCGGTGGTCTCCACG 626

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     627 GCGACCAAGATGTCGAGCTTTGGGCTCATCTCCTCTCAAACTCAGTACTTCTTGTCCTTG 686

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     687 TTGCTCTCCGACAAGGAGTTCACAGCGAACTACATAGCGGAGAACAAGAAGCGGCT-TAG 745

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     746 AGAGCGGCAAAAGCGGCTCACCGAAGCGCTGCGGACGATCGGTATAAACTGTTTGGAGAG 805

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     806 CAATGCAGGGT--TGTTTTGTTGGGTGGACATGAGGCACTTACTTAAGTCTAAGACACCT 863

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     864 GAAGGAGAGATGGAGCTGTGGAAAAGGATAGTGCATGATGTGGGACTAAACATTTCTCCG 923

Qy     361 GGTTCTT 367
Db     924 GGCTCTT 930


RESULT 6
AAV00219
ID   AAV00219 standard; DNA; 968 BP.
XX
AC   AAV00219;
XX
DT   08-JUN-1998  (first entry)
XX
DE   1-aminocyclopropane-1-carboxylic acid synthase gene acacc2.
XX
KW   1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
KW   flowering; inhibition; regulation; development; fruit; ss.
XX
OS   Ananas comosus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..968
FT                   /*tag=  a
FT                   /product= "acacc2"
FT                   /transl_except= (pos:967..968,aa:Val)
FT                   /note= "no stop codon given"
XX
PN   AU9719963-A.
XX
PD   06-NOV-1997.
XX
PF   01-MAY-1997;   97AU-0019963.
XX
PR   01-MAY-1996;   96AU-0009582.
XX
PA   (GOLD-) GOLDEN CIRCLE LTD.
PA   (QUEE-) STATE QUEENSLAND.
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Botella J,  Sanewski G;
XX
DR   WPI; 1998-009279/02.
DR   P-PSDB; AAW37444.
XX
PT   New isolated ACC synthase genes from pineapples - used to generate
PT   transgenic pineapples in which the natural initiation of flowering
PT   is inhibited
XX
PS   Claim 1; Fig 1; 37pp; English.
XX
CC   The present sequence represents the nucleotide sequence encoding a
CC   1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of
CC   pineapple. The present invention describes a transgenic variety of
CC   pineapple in which initiation of flowering is inhibited, the variety
CC   comprising a nucleotide sequence encoding an ACC synthase enzyme where
CC   the nucleotide sequence is operably linked, in the sense or antisense
CC   orientation, to one or more regulatory nucleotide sequences. The ACC
CC   synthase gene can be used to regulate pineapple plant development,
CC   particularly for inhibiting initiation of flowering. Such plants can
CC   then be induced to flower in a narrow spectrum of time which would
CC   thereby decrease the spread of fruit maturity within a crop.
XX
SQ   Sequence 968 BP; 241 A; 235 C; 294 G; 198 T; 0 other;

  Query Match             20.9%;  Score 84.6;  DB 19;  Length 968;
  Best Local Similarity   52.7%;  Pred. No. 4.7e-19;
  Matches  208;  Conservative    0;  Mismatches  184;  Indels    3;  Gaps    1;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     571 GGCCTCCCCGGTTTTAGGGTTGGGACGATCTATTCATACAACAATAGGGTGGTGACCACG 630

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     631 GCGAGGAGGATGTCGAGCTTCACACTCGTGTCGTCGCAGACTCAGAAGACGCTGGCGTCG 690

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     691 ATGCTGTCGGACGAGGAGTTCACAAAGTACTACATAAGGACCAACAGGGAGAGGCTGAAG 750

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     751 AGGAGGTACGAGTACATAATCCAGGGGCTGGAGAGAGCAGGGATTGAGTGCTTCCAAGGG 810

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     811 AATGCCGGGCTGTTC---TGCTGGATGAATCTGGGGCCACTCCTCGAGGAGCAGACGAGA 867

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     868 GAAGGGGAGCTCAGCCTGTGGAAACTGATATTGCATGAGGTGAGGCTCAACATATCACCA 927

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTT 395
Db     928 GGATCTTCATGCCACTGCTCTGAGCCTGGCTGGTT 962


RESULT 7
AAT66247
ID   AAT66247 standard; DNA; 1170 BP.
XX
AC   AAT66247;
XX
DT   28-JUL-1997  (first entry)
XX
```

```
DE   ACC synthase GAC-2 DNA.
XX
KW   ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense;
KW   ethylene; transgenic plant; Pelargonium x domesticum;
KW   in vitro propagation; tissue culture; ripening; ss.
XX
OS   Not identified.
XX
PN   WO9717429-A1.
XX
PD   15-MAY-1997.
XX
PF   08-NOV-1996;   96WO-US17954.
XX
PR   09-NOV-1995;   95US-0555755.
XX
PA   (OGLE-) OGLEVEE LTD.
PA   (PENN-) PENN STATE RES FOUND.
XX
PI   Arteca J,  Arteca RN,  Oglevee-O'Donovan W,  Stoots E;
XX
DR   WPI; 1997-281019/25.
DR   P-PSDB; AAW09879.
XX
PT   Commercial propagation of transgenic plants by tissue culture -
PT   especially Pelargonium x domesticum with decreased ethylene
PT   formation
XX
PS   Claim 14; Page 24; 36pp; English.
XX
CC   2 DNA sequences (AAT66246-47) respectively code for
CC   1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1
CC   (AAW09878) and GAC-2 (AAW09879), enzymes involved in the biosynthesis
CC   of ethylene in plants.  In a method for the commercial production
CC   of transgenic plants, Agrobacterium vectors carrying antisense
CC   genes for ACC synthase or ACC oxidase (see also AAT66248) are used
CC   to inoculate petiole explants of a mother plant, pref.
CC   Pelargonium x domesticum.  The resulting callus is cultured and
CC   used to regenerate transgenic plants.  The antisense genes prevent
CC   ACC synthase or ACC oxidase expression and hence ethylene
CC   formation and fruit ripening.
XX
SQ   Sequence 1170 BP; 319 A; 263 C; 297 G; 291 T; 0 other;

  Query Match             20.7%;  Score 83.6;  DB 18;  Length 1170;
  Best Local Similarity   53.7%;  Pred. No. 1.2e-18;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
             || || || || |||||| ||||  || ||||||||||||| ||    ||  | | |  |
Db     763 GGCTTCCCTGGCTTCAGGGTGGGGATTGTCTACTCCTACAATGACGCAGTTGTGAATTGT 822

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           ||   |||| || | || ||        | ||  | |  || |||| | |  |||
Db     823 GCGCGAAAGATGTCAAGTTTCGGCCTTGTATCCACACAAACTCAGCACCTAATCGCATCA 882

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||||||||||||      |||    | |  ||||||| ||  | |     ||  ||
Db     883 ATGCTCTCGGACGATGAATTCGTGGACACATTCATCGTGGAGAGCGCGAAGAGGCTAGCG 942

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           |||| ||||||  | |||      ||| ||| |  || ||  |||  |  ||    | ||
Db     943 AGAAGGTACGCAACCTTCACAAGAGGGCTTGCA-CAAGTCCACATTGGGAGCCTAAAGAG 1001

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  || || || |  ||   |||   ||| |||| |  |  |        | |
Db    1002 CAATGGGGGGTTATTCAT--ATGGATGGACTTGAGGAGGCTTCTCAAGGAGAAGACTTTC 1059

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            | |  ||| | |  || |||     | |  | ||    |  ||| |||| ||  | ||
Db    1060 GAGGCGGAGATGGCTCTGTGGAGAGTGATAATCAATGAGGTGAAGCTAAATGTGTCGCCA 1119

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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           ||  | |  |  |||||    || || || |  || ||  ||||
Db    1120 GGGGCGTCGTTCCATTGCTCGGAGCCAGGGTGGTTCAGAGTCTG 1163


RESULT 8
AAV30326
ID   AAV30326 standard; cDNA; 1878 BP.
XX
AC   AAV30326;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA.
XX
KW   ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
KW   ethylene; transgenic plant; wilting; geranium; pPHSacc49; ss.
XX
OS   Pelargonium x hortorum cv. Sincerity.
XX
FH   Key             Location/Qualifiers
FT   CDS             104..1576
FT                   /*tag= a
FT   polyA_signal    1810..1815
FT                   /*tag= b
FT   misc_feature    complement (1..50)
FT                   /*tag= c
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (51..100)
FT                   /*tag= d
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (101..150)
FT                   /*tag= e
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (151..200)
FT                   /*tag= f
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (201..250)
FT                   /*tag= g
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (251..300)
FT                   /*tag= h
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (301..350)
FT                   /*tag= i
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (351..400)
FT                   /*tag= j
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (401..450)
FT                   /*tag= k
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (451..500)
FT                   /*tag= l
FT                   /note= "antisense oligonucleotide (Claim 13)"
FT   misc_feature    complement (1..1878)
FT                   /*tag= m
FT                   /note= "any contiguous 50 nucleotides (Claim 13)"
XX
PN   WO9814465-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17644.
XX
PR   01-OCT-1996;   96US-0724194.
XX
PA   (COLS ) UNIV COLORADO STATE RES FOUND.
XX
PI   Ranu RS;
XX
DR   WPI; 1998-260994/23.
DR   P-PSDB; AAW60235.
XX
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```
PT   New isolated ACC synthase genes - are obtained from geranium and
PT   rose, used to develop products for producing plants with reduced
PT   ethylene levels, for increasing shelf-life
XX
PS   Claim 1; Fig 5; 77pp; English.
XX
CC   This cDNA clone, designated pPHSacc49 (ATCC 98179), codes for a
CC   55.1 kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase)
CC   (see AAW60235) of geranium (Pelargonium x hortorum cv. Sincerity).
CC   High quality mRNA was obtained from flower tissue using a novel
CC   adaptation of the 2-butoxyethanol precipitation technique.  This
CC   was converted to cDNA and screened with a probe generated by PCR
CC   amplification (see AAV30328-29).  The pPHSacc49 clone was obtained.
CC   Geranium ACC synthase cDNA clones pHSacc41 (see AAV30324) and
CC   pPHSacc44 (see AAV30325), and rose ACC synthase cDNA clone pRoseKacc7
CC   (see AAV30330), are also claimed.  These ACC synthase genes, or their
CC   fragments, when introduced in antisense orientation under control
CC   of a strong promoter, can be used to genetically modify a plant,
CC   especially geranium, rose or woody plant.  As a consequence, the
CC   amount of ACC synthase produced in the plant cells is reduced and
CC   the rate of ACC conversion to ethylene decreases.  This can be used
CC   to prolong the shelf-life of cut flowers and to reduce leaf
CC   yellowing and petal abscission during shipping and storage.
XX
SQ   Sequence 1878 BP; 569 A; 390 C; 432 G; 487 T; 0 other;

  Query Match             20.7%;  Score 83.6;  DB 19;  Length 1878;
  Best Local Similarity   53.7%;  Pred. No. 1.5e-18;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     953 GGCTTCCCTGGCTTCAGGGTGGGGATTGTCTACTCCTACAATGACGCAGTTGTGAATTGT 1012

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db    1013 GCGCGAAAGATGTCAAGTTTCGGCCTTGTATCCACACAAACTCAGCACCTAATCGCATCA 1072

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db    1073 ATGCTCTCGGACGATGAATTCGTGGACACATTCATCGTGGAGAGCGCGAAGAGGCTAGCG 1132

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db    1133 AGAAGGTACACAACCTTCACAAGAGGGCTTGCA-CAAGTGAACATTGGATGCCTAAAGAG 1191

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db    1192 CAATGGGGGGTTATTCAT--ATGGATGGACTTGAGGAGGCTTCTCAAGGAGAAGACTTTC 1249

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db    1250 GAGGCGGAGATGGCTCTGTGGAGAGTGATAATCAATGAAGTGAAGCTAAATGTGTCGCCA 1309

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1310 GGGGCGTCGTTCCATTGCTCGGAGCCAGGGTGGTTTAGAGTGTG 1353


RESULT 9
AAT33139
ID   AAT33139 standard; cDNA; 993 BP.
XX
AC   AAT33139;
XX
DT   07-DEC-1996  (first entry)
XX
DE   Broccoli ACC synthase cDNA clone TA13.
XX
KW   ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;
KW   ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
KW   antisense; broccoli; ss.
XX
OS   Brassica oleracea.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     3..992
FT                   /*tag=  a
FT   primer_bind     complement (1..14)
FT                   /*tag=  b
FT                   /note= "primer RMM494"
FT   primer_bind     975..993
FT                   /*tag=  c
FT                   /note= "primer RMM491"
XX
PN   WO9621027-A1.
XX
PD   11-JUL-1996.
XX
PF   07-JUN-1995;   95WO-US07271.
XX
PR   30-DEC-1994;   94US-0366992.
XX
PA   (ASGR-) ASGROW SEED CO.
XX
PI   Boeshore ML,  Carney KJ,  Deng RZ,  Reynolds JF,  Ruttencutter GE;
XX
DR   WPI; 1996-334002/33.
DR   P-PSDB; AAR98599.
XX
PT   DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of
PT   Brassica oleracea  - used to regulate ethylene-dependent processes
PT   in plants, esp. to improve shelf life
XX
PS   Claim 3; Fig6A-C; 50pp; English.
XX
CC   Brassica oleracea cDNA clone TA13 (AAT33137) codes for
CC   1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
CC   (AAR98599), an enzyme involved in ethylene biosynthesis.  It was
CC   obtd. by PCR amplification (see also AAT33140) of broccoli floret
CC   cDNA.   The PCR product was cloned into pCRII to obtain clone
CC   TA31.  cDNA or genomic DNA (see also AAT33136) can be inserted, in
CC   sense or antisense orientation, into an expression cassette and then
CC   transferred to a binary vector suitable for Agrobacterium-mediated
CC   plant transformation.  The constructs permit control of the level of
CC   ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
CC   melo) and hence a control of maturation, ageing and shelf-life.
XX
SQ   Sequence 993 BP; 269 A; 233 C; 253 G; 238 T; 0 other;

  Query Match             20.3%;  Score 82.2;  DB 17;  Length 993;
  Best Local Similarity   55.0%;  Pred. No. 3.3e-18;
  Matches  203;  Conservative    0;  Mismatches  163;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     621 GGTCTTCCCGGTTTTCGAGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA 680

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     681 GCGAGAAGGATGTCGAGTTTCACGCTTGTCTCGTCTCAGACACAACACATGTTGGCTTCC 740

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     741 ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 800

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     801 AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG 859

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     860 TAATGCAGGGT--TGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA 917

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
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Db    918 CAAGGCGAGCTCGAGCTTTTGGGTGTGATCTTGAAGGAACTAAAGCTGAATATATCTCCT 977

Qy    361 GGTTCTTGT 369
          | |  | ||
Db    978 GATCTTCGT 986


RESULT 10
AAT73502
ID   AAT73502 standard; cDNA to mRNA; 1868 BP.
XX
AC   AAT73502;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2.
XX
KW   Ozone; induction; exposure; resistance; transgenic plant; ACC;
KW   1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
XX
OS   Poplar nigra.
XX
FH   Key             Location/Qualifiers
FT   CDS             119..1579
FT                   /*tag=  a
FT                   /product= PNACCS2
XX
PN   JP09075088-A.
XX
PD   25-MAR-1997.
XX
PF   07-SEP-1995;   95JP-0254510.
XX
PR   07-SEP-1995;   95JP-0254510.
XX
PA   (TOYT ) TOYOTA JIDOSHA KK.
XX
DR   WPI; 1997-239270/22.
DR   P-PSDB; AAW21755.
XX
PT   Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT   enzyme genes  - from poplar tree, are useful for generating
PT   ozone-resistant trees and pollution clean-up trees
XX
PS   Claim 2; Pages 9-11; 12pp; Japanese.
XX
CC   This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-
CC   carboxylic acid (ACC) synthase gene isolated from poplar trees which
CC   had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC   for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC   humidity, 30 k lux and air current 30 cm/second. This gene will be
CC   useful for breeding air pollutant ozone-resistant trees, especially
CC   poplar.
XX
SQ   Sequence 1868 BP; 590 A; 366 C; 405 G; 507 T; 0 other;

  Query Match             20.3%;  Score 82;  DB 18;  Length 1868;
  Best Local Similarity   53.5%;  Pred. No. 5.4e-18;
  Matches  216;  Conservative    0;  Mismatches  185;  Indels    3;  Gaps    2;

Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
            ||  | || || |||||  | ||  || | ||||| ||||||||    ||  | | |
Db    944 GGACTCCCTGGCTTCAGAGTTGGAATTGTTTACTCATACAACGATGCAGTTGTTAATTGC 1003

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          | |  |||| || | || |||       | ||  | |  ||  ||    || || |
Db   1004 GGCCGAAAGATGTCAAGTTTTGGTCTGGTCTCCTCACAAACTCAATATTTACTTGCTTCA 1063

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||||| || ||      |||     |  | ||| | |  |  | |     ||  || ||
Db   1064 ATGCTTTCTGATGAAGAGTTTGTCGAGGATTTCCTAGCCGAGAGCTCGAAGAGGCTAAAG 1123

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
          | || | ||| |   |||     |||  | ||| ||| | || ||| | ||   ||||||
Db   1124 AAAAGGCACGGTATTTTCACAAAGGGATTGGAACAAA-TTGGGATCAGTTGTTTGGAAAG 1182

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          ||  |  ||  ||||| |  |||     |  || ||    |  ||       | |   |
Db   1183 CAAAGCCGG--TCTCTTTGTTTGGATGAATTTGCGCCATCTCCTTAAGGAACAAACAAAT 1240

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
          | || ||  | || || |||     | |  | ||    |  ||| |||| ||| | ||
Db   1241 GATGGTGAAATGGAACTGTGGCGTGTGATCGTTAATGACGTGAAGCTAAATGTTTCGCCA 1300

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          || ||||  |  ||||| |||| || || |  ||||| ||||
Db   1301 GGCTCTTCCTTCCATTGCGTTGAGCCTGGTTGGTTTAGGGTCTG 1344


RESULT 11
AAT73501
ID   AAT73501 standard; cDNA to mRNA; 1864 BP.
XX
AC   AAT73501;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS1.
XX
KW   Ozone; induction; exposure; resistance; transgenic plant; ACC1;
KW   1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
XX
OS   Poplar nigra.
XX
FH   Key             Location/Qualifiers
FT   CDS             194..1639
FT                   /*tag=  a
FT                   /product= PNACCS1
XX
PN   JP09075088-A.
XX
PD   25-MAR-1997.
XX
PF   07-SEP-1995;   95JP-0254510.
XX
PR   07-SEP-1995;   95JP-0254510.
XX
PA   (TOYT ) TOYOTA JIDOSHA KK.
XX
DR   WPI; 1997-239270/22.
DR   P-PSDB; AAW21754.
XX
PT   Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT   enzyme genes  - from poplar tree, are useful for generating
PT   ozone-resistant trees and pollution clean-up trees
XX
PS   Claim 2; Pages 7-9; 12pp; Japanese.
XX
CC   This sequence, designated PNACCS1, is a 1-aminocyclopropane-1-
CC   carboxylic acid (ACC) synthase gene isolated from poplar trees which
CC   had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC   for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC   humidity, 30 k lux and air current 30 cm/second. This gene will be
CC   useful for breeding air pollutant ozone-resistant trees, especially
CC   poplar.
XX
SQ   Sequence 1864 BP; 574 A; 360 C; 392 G; 538 T; 0 other;

  Query Match             20.0%;  Score 80.8;  DB 18;  Length 1864;
  Best Local Similarity   50.0%;  Pred. No. 1.4e-17;
  Matches  202;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
          ||  || || ||  |||||  | ||| |||||||  || |||||  ||    ||  | | |
Db   1025 GGCTTCCCTGGCCTCAGGGTTGGCATTATCTATTCTTACAATGATGCAGTTGTGAGTTGC 1084
```

```
Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           |||   ||| || | || ||   ||   | ||  | |  || |||  | || | |
Db    1085 GCCCGCAAGATGTCAAGCTTCGGATTGGTATCCACACAAACTCAGTACCTGATAGCATCA 1144

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||||| ||||| |     ||      | | ||||||   || || || |  || | |
Db    1145 ATGCTATCGGATAATGAATTTGTGGAGATGTTCATTAGGGAAAGCAAAAGGAGATTAGCC 1204

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             || |||    |  |||      ||  ||||  ||   |   |  |          |
Db    1205 GCAAGGTATAGAGTCTTCACTCGTGGACTTGATCAAGTAGGCATTGAGTGTTTGAAGACA 1264

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
                   || | ||  |||   ||  ||||  || |  |   |    |    | |
Db    1265 AGTAATGCTGGCCTGTTTTTGTGGATGGATTTGAGTAGACTCCTCAAACAGCAGACATTT 1324

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           ||||  ||  | || ||||||       |  |  |    |  ||| | |||||| | ||
Db    1325 AAAGCTGAAATGGAACTATGGCGAGTTATAATCCATGAAGTCAAGCTCAACGTTTCGCCG 1384

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||||  | || ||||||  |  | || || |  |||||  | ||
Db    1385 GGTTGCTCTTTTCATTGCTTGAAGCCAGGGTGGTTTAGGGTTTG 1428


RESULT 12
AAT72631
ID   AAT72631 standard; DNA; 1096 BP.
XX
AC   AAT72631;
XX
DT   27-JAN-1998  (first entry)
XX
DE   Mangifera indica ACC synthase miacc1 gene.
XX
KW   ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW   miacc1; ethylene biosynthesis; transgenic plant; senescence;
KW   antisense expression system; plant development; fruit ripening;
KW   EC 4.4.1.14; mango; multigene family; ss.
XX
OS   Mangifera indica.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1096
FT                   /*tag=  a
FT                   /product= miacc1
FT                   /EC_number= 4.4.1.14
FT                   /note= "Sequence represents 75% of the coding
FT                          sequence and does not contain the start
FT                          or stop codons."
XX
PN   WO9711166-A1.
XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-AU00591.
XX
PR   02-MAY-1996;   96AU-0009603.
PR   20-SEP-1995;   95AU-0005559.
XX
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Botella JR;
XX
DR   WPI; 1997-202875/18.
DR   P-PSDB; AAW18289.
XX
PT   Pineapple, papaya and mango ACC synthase genes - used in gene
PT   therapy to produce fruits with reduced senescence
XX
PS   Claim 4; Fig 4; 46pp; English.
XX
CC   This sequence represents a novel gene, miacc1, which is a member
CC   of an ACC synthase multigene family found in mango. ACC synthase is
CC   involved in the pathway for ethylene biosynthesis and the rate of
CC   endogenous expression of ACC synthase is considered to limit
CC   substantially the rate of ethylene production. Endogenous ethylene is
CC   often deleterious to crops, especially if some form of mechanical
CC   wounding has occurred and diminishes their post harvest quality and
CC   storage life. Novel ACC synthase genes expressed in transgenic plants
CC   using either sense or antisense expression system may be used to control
CC   the regulation of plant development, in particular fruit ripening,
CC   reducing senescence and thus improving storage life.
XX
SQ   Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;

  Query Match             19.9%;  Score 80.4;  DB 18;  Length 1096;
  Best Local Similarity   53.2%;  Pred. No. 1.5e-17;
  Matches  215;  Conservative    0;  Mismatches  186;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || || ||| | ||| || | || || || || ||    ||  | | |  |
Db     688 GGCCTCCCTGGCTTTAGGGTTGGCATTGTTTATTCTTATAATGATGCAGTTGTGAGTTGT 747

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
             |   ||| || | || ||    |   | ||  | |  || ||    || ||||
Db     748 ATCCGCAAGATGTCAAGCTTCGGTTTGGTATCCTCACAAACTCAATATTTACTCGCTTCA 807

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||||| || ||        ||     |||||||  | | || || | |  || ||   |
Db     808 ATGCTTTCTGATGATGAATTTGTGGAAAAGTTTCTAGCGGAAAGCTCAAAGAGGCTGGCA 867

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           | || ||||  |   |||     | |  ||| ||||| | || ||    |||  | |  |
Db     868 AAAAGGTACCATATTTTCACAAAGAGACTTG-AGAAAGTGGGGATTAACTGCTTGAAGGG 926

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
             |  | |||  |||  |  |  |||   ||  || |     |  |||  |    | |  |
Db     927 AAATGCAGG--TCTTTTCTTCTGGATGGATTTGCGACACCTCCTTCAACAAGAAACAGTT 984

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           | |  ||  |  |||||||| || | |  | |||  ||  ||  | ||||| | ||
Db     985 GATGCCGAAATGAAGCTATGGGGCACGATTTTGAACGATGTGAAACTTAACGTTTCACCA 1044

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || ||||  | ||||||    || || || |  || ||  ||||
Db    1045 GGCTCTTCCTTTCATTGCCAGGAGCCTGGTTGGTTCAGAGTCTG 1088


RESULT 13
AAT72632
ID   AAT72632 standard; DNA; 1113 BP.
XX
AC   AAT72632;
XX
DT   27-JAN-1998  (first entry)
XX
DE   Mangifera indica ACC synthase miacc2 gene.
XX
KW   ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW   miacc2; ethylene biosynthesis; transgenic plant; senescence;
KW   antisense expression system; plant development; fruit ripening;
KW   EC 4.4.1.14; mango; multigene family; ss.
XX
OS   Mangifera indica.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1113
FT                   /*tag=  a
FT                   /EC_number= 4.4.1.14
FT                   /product= miacc2
FT                   /note= "Sequence represents 75% of the coding
FT                          sequence and does not contain the start
FT                          or stop codons."
XX
PN   WO9711166-A1.
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XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-AU00591.
XX
PR   02-MAY-1996;   96AU-0009603.
PR   20-SEP-1995;   95AU-0005559.
XX
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Botella JR;
XX
DR   WPI; 1997-202875/18.
DR   P-PSDB; AAW18290.
XX
PT   Pineapple, papaya and mango ACC synthase genes - used in gene
PT   therapy to produce fruits with reduced senescence
XX
PS   Claim 5; Fig 5; 46pp; English.
XX
CC   This sequence represents the novel gene, miacc2, which is a member
CC   of the mango ACC synthase multigene family. ACC synthase an enzyme
CC   involved in the pathway for ethylene biosynthesis and the rate of
CC   endogenous expression of ACC synthase is considered to limit
CC   substantially the rate of ethylene production. Endogenous ethylene is
CC   often deleterious to crops, especially if some form of mechanical
CC   wounding has occurred and diminishes their post harvest quality and
CC   storage life. Novel ACC synthase genes expressed in transgenic plants
CC   using either sense or antisense expression system may be used to control
CC   the regulation of plant development, in particular fruit ripening,
CC   reducing senescence and thus improving storage life.
XX
SQ   Sequence 1113 BP; 320 A; 212 C; 264 G; 317 T; 0 other;

  Query Match             19.9%;  Score 80.4;  DB 18;  Length 1113;
  Best Local Similarity   53.2%;  Pred. No. 1.5e-17;
  Matches  215;  Conservative    0;  Mismatches  186;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||||| || || || ||| | ||| |||| ||||| |||||||| |  ||  | | |
Db     694 GGGTTCCCAGGCTTTAGGGTCGGCATTATATACTCATACAACGATACAGTTGTGAGTTGC 753

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           |||   ||  || | || |||  |    | ||| | |  || || |  ||  |||
Db     754 GCCTGCAAAATGTCAAGCTTTGGACTTGTATCATCACAAACTCAACATTTAATCGCTTCA 813

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||| | || ||       ||     | | ||||||    |  |        |  ||   |
Db     814 ATGTTATCAGATGATGAATTTGTGGATAGGTTCATTACTGAGAGTGCTAAAAGGCTTGCA 873

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           | || | ||   || |||     ||||| |     || | |||||  | ||   | | ||
Db     874 AAAAGGCACAGAGCCTTC-ACATGGGGGCTATCTCAAGTAGGCATTGGTTGTTTGAAGAG 932

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  |  ||   || | ||  |||   ||  ||       |  |        | |  ||
Db     933 CAATGCGGG--GCTATTTTTCTGGATGGATTTGCATCATCTCCTCAAGGAGCAAACTGAT 990

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            ||| |||| | || || ||| |   | |  | |||   | |||  |||| ||| ||||
Db     991 GAAGCAGAGATAGAACTGTGGAAAGTGATAATCAACGAAGTTAAATTAAATGTTTCTCCG 1050

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           |||||||  | ||||||   | | || || |  ||| |  | ||
Db    1051 GGTTCTTCCTTTCATTGCGCTAATCCAGGATGGTTTCGGGTTTG 1094


RESULT 14
AAX27501
ID   AAX27501 standard; cDNA; 1712 BP.
XX
AC   AAX27501;
XX
DT   26-MAY-1999  (first entry)
XX
DE   Banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) cDNA.
XX
KW   1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana;
KW   ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening;
KW   transgenic; enzyme; inhibition; flavour; texture; ss.
XX
OS   Musa sp.
XX
PN   US5886164-A.
XX
PD   23-MAR-1999.
XX
PF   15-APR-1996;   96US-0632598.
XX
PR   15-APR-1996;   96US-0632598.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Bird CR,  Fletcher JD;
XX
DR   WPI; 1999-228611/19.
XX
PT   Novel isolated cDNA molecules ((pASC6) and (pACOS7)) encoding
PT   1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene
PT   forming enzyme (EFE) - useful for modifying fruit ripening
PT   characteristics, especially in bananas
XX
PS   Claim 1; Columns 11-14; 22pp; English.
XX
CC   The invention relates to two isolated cDNA molecules ((pASC6) and
CC   (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS)
CC   and an ethylene forming enzyme (EFE), respectively. The clones are
CC   deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814,
CC   respectively. pASC6 and pACOS7 may be used to genetically control
CC   ethylene biosynthesis in plants and hence regulate the ethylene-induced
CC   processes involved in fruit ripening (and other ethylene related
CC   processes). Vectors comprising the cDNA sequences may be used to produce
CC   transgenic bananas with altered fruit ripening characteristics. The
CC   orientation of the pASC6 and pACOS7 used in the construct, will determine
CC   how the ripening process is affected. If the genes have a sense
CC   orientation, and transcribe mRNA that encodes an active enzyme, the rate
CC   of ripening will be increased (up-regulation) (however, full-length sense
CC   constructs can also be used to inhibit enzyme expression by co-
CC   inhibition). If genes encode antisense mRNA, they will inhibit the
CC   expression of the genes involved in fruit ripening and hence slow the
CC   process down (down-regulation). In this manner different spatial and
CC   temporal patterns of genes expression can be produced. Retardation of the
CC   rate of ripening will reduce the rate of deterioration of banana fruit
CC   after harvest. This helps in production of high quality fruit that has
CC   improved flavour and texture. The present sequence represents the cDNA
CC   sequence of the banana ACS enzyme.
XX
SQ   Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

  Query Match             19.5%;  Score 78.8;  DB 20;  Length 1712;
  Best Local Similarity   53.0%;  Pred. No. 6.9e-17;
  Matches  214;  Conservative    0;  Mismatches  187;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || ||| |  | ||||| || ||||||||||||||    |||| |||
Db     865 GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || |  ||| || |||| |||  |    | ||  | | ||||||| | ||||||
Db     925 GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||| |    |||  |  ||||||    |  ||| | | |   | | |  |||   |
Db     985 ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
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Db   1045 GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300

Db   1104 CAACGCGGG--GCTGTTCTGCTGGATGGACTTGAGGCCGTTGCTGAAGGAAGCGACGGTG 1161

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360

Db   1162 GAGGCGGACGTCCGGCTGTCGGCGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG 1221

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404

Db   1222 GGGTCGTCCTTCCACTGCTCGGAGCCGGGGTGGTTCAGGGTGTG 1265
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RESULT 15
AAS09901
ID AAS09901 standard; cDNA; 1712 BP.
XX
AC AAS09901;
XX
DT 24-OCT-2001 (first entry)
XX
DE DNA encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS).
XX
KW 1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana;
KW ethylene biosynthesis; ethylene-forming enzyme; EFE; fruit ripening;
KW fruit storage; ss.
XX
OS Musa sp.
XX
PN US6262346-B1.
XX
PD 17-JUL-2001.
XX
PF 15-JAN-1999; 99US-0231240.
XX
PR 15-APR-1996; 96US-0632598.
XX
PA (ZENE) ZENECA LTD.
XX
PI Bird CR, Fletcher JD;
XX
DR WPI; 2001-450497/48.
XX
PT Modifying level of ethylene biosynthesis in plant of genus Musa,
PT involves inserting into genome of plant a DNA sequence encoding banana
PT 1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming
PT enzyme -
XX
PS Claim 2; Column 13; 23pp; English.
XX
CC The sequence represents the coding sequence of 1-aminocyclopropane-1-
CC carboxylic acid synthase (ACS) from banana, used in the method of
CC the invention. The method involves modifying the level of ethylene
CC biosynthesis in a plant of the genus Musa by inserting into the genome of
CC the plant a DNA sequence (I) encoding a banana 1-aminocyclopropane-1-
CC carboxylic acid synthase (ACS) or an ethylene-forming enzyme (EFE), where
CC (I) is in sense or antisense configuration, and modifies the level of
CC activity of ACS or EFE. This retards the rate of ripening in banana
CC fruits which reduces the rate of deterioration of banana fruit after
CC harvest. As a result, fruit may be harvested when they have reached
CC partial or full ripeness and still have the robustness to withstand
CC handling and transport to reach the consumer in good condition. In this
CC way high quality ripe fruit can be made available to the consumer with
CC reduced requirement for post-harvest treatment. High quality fruit will
CC have improved flavour and texture. High quality fruit can be produced
CC consistently over a wide harvest period, and such fruit can be held in
CC store for long periods and ripened to optimal quality by the supply of
CC exogenous ethylene.
XX
SQ Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match 19.5%; Score 78.8; DB 22; Length 1712;
Best Local Similarity 53.0%; Pred. No. 6.9e-17;
Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

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Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60

Db    865 GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120

Db    925 GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180

Db    985 ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240

Db   1045 GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300

Db   1104 CAACGCGGG--GCTGTTCTGCTGGATGGACTTGAGGCCGTTGCTGAAGGAAGCGACGGTG 1161

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360

Db   1162 GAGGCGGACGTCCGGCTGTGGCGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG 1221

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404

Db   1222 GGGTCGTCCTTCCACTGCTCGGAGCCGGGGTGGTTCAGGGTGTG 1265
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GenCore version 5.1.3

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	196.4	48.6	894	8	AF184076	AF184076 Prunus ar
2	178	44.1	581	8	AF146028	AF146028 Actinidia
3	147.8	36.6	1674	8	AF348575	AF348575 Arabidops
4	147.8	36.6	1757	8	AY054691	AY054691 Arabidops
c 5	147.8	36.6	98412	8	F16P17	AC011000 Sequence
6	146.8	36.3	1089	8	TAU35779	U35779 Triticum ae
7	144.2	35.7	143113	8	AP000559	AP000559 Oryza sat
8	127.6	31.6	1488	8	AF336920	AF336920 Arabidops
c 9	127.6	31.6	86212	8	AB010074	AB010074 Arabidops
10	117.2	29.0	1372	8	MSBACS2GE	X96947 Musa acumin
11	114	28.2	1812	8	MSBACS1GE	X96946 M.acuminata
12	110.8	27.4	1400	8	AF312737	AF312737 Malus x d
13	110.8	27.4	1618	8	MSU03294	U03294 Malus sylve
14	110.8	27.4	1633	8	MDO011518	AJ011518 Malus dom
15	110.8	27.4	1778	8	AB015624	AB015624 Pyrus pyr
16	110.8	27.4	1812	8	PCPCACS1G	X87112 P.communis
17	110.8	27.4	2004	8	MAUACCSYN	L31347 Malus domes
18	110.8	27.4	5526	8	MDU89156	U89156 Malus domes
19	109.2	27.0	1840	8	VRU34987	U34987 Vigna radia
20	109.2	27.0	4405	8	AF151961	AF151961 Vigna rad
21	107.6	26.6	1344	8	AF332390	AF332390 Arabidops
22	107.6	26.6	5676	8	AB010102	AB010102 Malus dom
23	107.6	26.6	89904	8	ATT25K17	AL049171 Arabidops
24	107.6	26.6	196286	8	ATCHRIV64	AL161564 Arabidops
25	106	26.2	3758	8	AF049711	AF049711 Petunia x
26	104.8	25.9	1413	8	AF334720	AF334720 Arabidops
27	104.8	25.9	1413	8	ATHACS5B	L29261 Arabidopsis
28	104.8	25.9	1873	8	AB000679	AB000679 Vigna rad
29	104.8	25.9	1892	8	VRU34986	U34986 Vigna radia
30	104.8	25.9	3234	8	NTA131837	AJ131837 Nicotiana
31	104.8	25.9	4284	8	ATHACS5A	L29260 Arabidopsis
32	104.8	25.9	4714	8	AB018355	AB018355 Vigna rad
c 33	104.8	25.9	84440	8	AB010075	AB010075 Arabidops
34	104.8	25.9	118086	8	ATF6H11	AL021684 Arabidops
35	103	25.5	1089	8	AB021908	AB021908 Musa acum
36	102.8	25.4	1410	8	AF334712	AF334712 Arabidops
37	102.8	25.4	1413	8	AF332391	AF332391 Arabidops
38	102.8	25.4	1638	8	CUCACCA	D01033 Cucurbita m
39	102.8	25.4	4346	8	CMU37774	U37774 Cucurbita m
c 40	102.8	25.4	97711	8	ATT16K5	AL132965 Arabidops
41	102.8	25.4	110766	8	ATT28I19	AL035709 Arabidops
42	102.8	25.4	198493	8	ATCHRIV88	AL161592 Arabidops
43	101.2	25.0	1115	8	AF338651	AF338651 Brassica
44	101.2	25.0	1393	8	VIRACCSYNT	M94863 Vigna radia
45	101.2	25.0	1393	8	VRACCSYN5	Z12134 V.radiata g

ALIGNMENTS

RESULT 1
AF184076
LOCUS AF184076 894 bp DNA linear PLN 01-OCT-2000
DEFINITION Prunus armeniaca ACC synthase (ACS1) gene, partial cds.
ACCESSION AF184076
VERSION AF184076.1 GI:10441264
KEYWORDS .
SOURCE Prunus armeniaca.
ORGANISM Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE 1 (bases 1 to 894)
AUTHORS Mbeguie-A-Mbeguie,D. and Fils-Lycaon,B.R.
TITLE Molecular cloning and nucleotide sequence of genomic DNA encoding

```
            ACC synthase from apricot fruit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 894)
  AUTHORS   Mbeguie-A-Mbeguie,D. and Fils-Lycaon,B.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-1999) Station de Technologie des Produits
            Vegetaux, Institut National de la Recherche Agronomique,
            Agroparc-Domaine Saint Paul, Avignon 84914, France
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Prunus armeniaca"
                     /db_xref="taxon:36596"
     gene            <1. .>894
                     /gene="ACS1"
     mRNA            join(<1. .35,123. .>894)
                     /gene="ACS1"
                     /product="ACC synthase"
     CDS             join(<1. .35,123. .>894)
                     /gene="ACS1"
                     /note="PA-ACS1"
                     /codon_start=1
                     /product="ACC synthase"
                     /protein_id="AAG16977.1"
                     /db_xref="GI:10441265"
                     /translation="DAFLVPTPYYPGLDKDIKWRTGVEIITVPCRSADKFNLSVTALD
                     RAFNQAKKRGLKVRGIIISNPSNPVGTLFSRESLYNLLDFAREKNIHIISNELFAGST
                     HGSEEFVSMADIVELEDLDQNRVHIVYGLSKDLSLPGFRAGVIYSFNKNVLAAAKRLT
                     RFSSISTPSQQLLSSMLSDTKFVQKFIDANRERLRGMHLKFLTGLKQLGIECTKSNGG
                     FSCWADMSGLIRSYNEKGELELWDRLLNVAKVNVTPGSSCHCIEPGWFRVW"
BASE COUNT      250 a    177 c    204 g    263 t
ORIGIN
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Query Match 48.6%; Score 196.4; DB 8; Length 894;
Best Local Similarity 71.5%; Pred. No. 1.2e-51;
Matches 286; Conservative 0; Mismatches 111; Indels 3; Gaps 2;

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Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
Db     497 TTCCAGGTTTTAGGGCGGGTGTTATCTACTCCTTTAACAAGAATGTGCTGGCTGCTGCTA 556

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
Db     557 AAAGGTTAACAAGGTTCTCGTCCATTTCCACTCCATCCCAACAGTTGCTCAGCTCTATGC 616

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
Db     617 TTTCAGACACCAAATTTGTCCAAAAGTTTATTGATGCCAATAGAGAGAGACTTCGAGGAA 676

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
Db     677 TGCACCTTAAATTTCTGAC-AGGGTTGAAGCAATTGGGCATTGAGTGTACAAAGAGCAAT 735

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
Db     736 GGAGG--TTTCAGCTGTTGGGCAGACATGAGTGGGTTAATCCGCTCTTACAATGAGAAAG 793

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
Db     794 GGGAGCTTGAGCTCTGGGATAGGTTGTTGAATGTAGCTAAGGTAAATGTAACTCCCGGAT 853

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db     854 CTTCATGTCATTGTATTGAACCCGGCTGGTTCCGCGTCTG 893
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RESULT 2
AF146028
LOCUS       AF146028                581 bp    DNA     linear   PLN 17-MAY-1999
DEFINITION  Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 3
            gene, partial cds.
ACCESSION   AF146028
VERSION     AF146028.1  GI:4836802
KEYWORDS    .
SOURCE      Actinidia chinensis.
  ORGANISM  Actinidia chinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; Ericales; Actinidiaceae; Actinidia.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Xu,C., Chen,K., Chen,D. and Zhang,S.
  TITLE     Molecular cloning of four members of ACC synthase gene family from
            kiwifruit (Actinidia chinensis Planch.)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 581)
  AUTHORS   Xu,C., Chen,D., Chen,K. and Zhang,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-1999) Department of Horticulture, Huajiachi
            Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang
            310029, People's Republic of China
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Actinidia chinensis"
                     /db_xref="taxon:3625"
                     /note="Actinidia chinensis Planch"
     CDS             <1. .>581
                     /note="ACS3"
                     /codon_start=3
                     /product="1-aminocyclopropane-1-carboxylate synthase 3"
                     /protein_id="AAD30563.1"
                     /db_xref="GI:4836803"
                     /translation="LLNRETLNTLLDFATEKNIHIISNEILASYSRESEEFVSLVEII
                     DSEDFDRNRVHIVYGLSKDLSLIGFGMGVIYSFNENVLSASKKLTRFASISAPTQHLL
                     ISMLSDTNFVDKFIKTNRERLHRICSEFVVGLKRLGIECAKSNAGFYCWADMRWLICS
                     YSEKGERKLWDKLLNVAKVNVTPGSSCHCIEPG"
BASE COUNT      166 a    112 c    132 g    171 t
ORIGIN
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Query Match 44.1%; Score 178; DB 8; Length 581;
Best Local Similarity 70.3%; Pred. No. 9e-46;
Matches 267; Conservative 0; Mismatches 110; Indels 3; Gaps 2;

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Qy      10 GGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCAAAAAG 69
Db     204 GGTTTCGGGATGGGGGTTATCTACTCCTTCAATGAGAATGTACTGTCTGCTTCGAAAAAA 263

Qy      70 TTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCTCG 129
Db     264 CTAACAAGATTCGCATCTATTTCAGCTCCAACCCAACACTTGCTTATCTCAATGCTTTCT 323

Qy     130 GACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTAC 189
Db     324 GATACAAATTTCGTCGATAAGTTTATCAAGACAAATCGAGAAAGGCTCCACCGGATTTGC 383

Qy     190 GCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGG 249
Db     384 AGTGAGTTTGTTG-TTGGGTTGAAGCGATTAGGTATAGAATGCGCAAAAAGCAATGCGGG 442

Qy     250 CTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGAG 309
Db     443 --TTTCTATTGTTGGGCTGACATGCGCTGGTTGATCTGCTCATACAGTGAGAAAGGCGAG 500

Qy     310 CTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTTGT 369
Db     501 CGAAAGCTCTGGGATAAGTTGTTGAATGTAGCTAAGGTTAATGTAACTCCTGGATCTTCC 560

Qy     370 TGTCATTGTATTGAACCCGG 389
Db     561 TGTCACTGTATTGAACCTGG 580
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RESULT 3
AF348575
LOCUS       AF348575                1674 bp    mRNA    linear   PLN 18-APR-2002
DEFINITION  Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase
            ACS10 (At1g62960) mRNA, complete cds.
ACCESSION   AF348575
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VERSION     AF348575.1  GI:13194767
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1674)
  AUTHORS   Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,
            Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,
            Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
            Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
            Theologis,A.
  TITLE     Arabidopsis Open Reading Frame (ORF) Clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1674)
  AUTHORS   Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
            Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Brooks,S.,
            Chao,Q., Chen,H., Cheuk,R., Karlin-Neumann,G., Kim,C., Lam,B.,
            Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
FEATURES             Location/Qualifiers
     source          1. .1674
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="C00005"
                     /note="This clone is in pUNI-T3-D/V5-His-TOPO.
                     ecotype: Columbia"
     gene            1. .1674
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     CDS             1. .1674
                     /gene="At1g62960"
                     /codon_start=1
                     /evidence=experimental
                     /product="1-aminocyclopropane-1-carboxylate synthase
                     ACS10"
                     /protein_id="AAK15546.1"
                     /db_xref="GI:13194768"
                     /translation="MTRTEPNRSRSSNSDSDKNSGNVGGGRTTGMRVIVPLQGVVQGR
                     GGLFLGSVIPCAFFYFLQFYLKRNRKNDESDNSGEQNSSASSSSSPNSGLPDPTRSQS
                     AGHLTELTGLPRSLSRILLSPRNSGGAVSVSGRVNCVLKGGDSSPYYVGQKRVEDDPY
                     DELGNPDGVIQLGLAQNNKLSLDDWVLENPKEAISDGLSISGIASYEPSDGLLELKMA
                     VAGFMTEATKNSVTFDPSQLVLTSGASSAIEILSFCLADSGNAFLVPTPCSPGYDRDV
                     KWRTGVDIIHVPCRSADNFNMSMVVLDRAFYQAKKRGVRIRGIIISNPSNPMGSLLSR
                     ENLYALLDFARERNIHIISNEIFAGSVHGEEGEFVSMAEIVDTEENIDRERVHIVYDL
                     SKDLSFRGLRSAAIYSFNESVLSASRKLTTLSPVSSPTQHLLISAISNPKNVQRFVKT
                     NRQRLQSIYTELVEGLKELGIECTRSNGGFYCWADMRGLISSYSEKGEIELWNKLLNI
                     GKINVIPGSCCHCIEPGWFRICFSNLSERDVPVVMNRIRKVCETCKSQN"
BASE COUNT      443 a    343 c    403 g    485 t
ORIGIN

  Query Match           36.6%;  Score 147.8;  DB 8;  Length 1674;
  Best Local Similarity   63.3%;  Pred. No. 5.2e-36;
  Matches  256;  Conservative    0;  Mismatches  142;  Indels    3;  Gaps    2;

Qy       4 TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
           || | |||| | ||    |  | ||||||||| | ||||||||  ||  |  |  || |
Db    1192 TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 1251

Qy      64 AAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATG 123
           | |||| | ||||   | ||| |  | ||| |||| || || |  |||||  |
Db    1252 AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 1311

Qy     124 CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
            ||||  |  |         ||| |  ||  |  |    |||||   || | |  | ||
Db    1312 ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 1371

Qy     184 ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
           || ||| | |   |||||| |||||||||  |  | || |||   |||||   |||||

Db    1372 ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 1430

Qy     244 CGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAA 303
           |||||  |  |||| |||||||| || ||| | |||||||||  ||| ||||||||||||
Db    1431 TGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTGATTTCATCTTACAGCGAAAAA 1488

Qy     304 GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGT 363
           || ||| | ||||| ||| ||||| |  | |||||||  ||| | || || |  || ||
Db    1489 GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 1548

Qy     364 TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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Db    1549 TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG 1589


RESULT 4
AY054691
LOCUS       AY054691                1757 bp    mRNA    linear   PLN 05-SEP-2001
DEFINITION  Arabidopsis thaliana Strong similarity to ACS5 from Lupinus albus
            gb|AF119414, and contains an Aminotransferase-classI domain
            PF|00155 (At1g62960; F16P17.11) mRNA, complete cds.
ACCESSION   AY054691
VERSION     AY054691.1  GI:15451221
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1757)
  AUTHORS   Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-2001) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence:  arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members  carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : ''RIKEN
            Arabidopsis  Full-Length cDNA''): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M.,  Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and  Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out  the
            sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
            Southwick,A.,  Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T.,  Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K.,  Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and  Davis,R.W.

            Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
     source          1. .1757
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                     /db_xref="taxon:3702"
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                     /clone="RAFL04-20-B08"
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     gene            1. .1757
                     /gene="At1g62960; F16P17.11"
     CDS             39. .1712
                     /gene="At1g62960; F16P17.11"
                     /codon_start=1
                     /product="Strong similarity to ACS5 from Lupinus albus
                     gb|AF119414, and contains an Aminotransferase-classI
                     domain PF|00155"
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                     /db_xref="GI:15451222"
                     /translation="MTRTEPNRSRSSNSDSDKNSGNVGGGRTTGMRVIVPLQGVVQGR
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                     AGHLTELTGLPRSLSRILLSPRNSGGAVSVSGRVNCVLKGGDSSPYYVGQKRVEDDPY
                     DELGNPDGVIQLGLAQNNKLSLDDWVLENPKEAISDGLSISGIASYEPSDGLLELKMA
                     VAGFMTEATKNSVTFDPSQLVLTSGASSAIEILSFCLADSGNAFLVPTPCSPGYDRDV
                     KWRTGVDIIHVPCRSADNFNMSMVVLDRAFYQAKKRGVRIRGIIISNPSNPMGSLLSR
                     ENLYALLDFARERNIHIISNEIFAGSVHGEEGEFVSMAEIVDTEENIDRERVHIVYDL
                     SKDLSFRGLRSAAIYSFNESVLSASRKLTTLSPVSSPTQHLLISAISNPKNVQRFVKT
                     NRQRLQSIYTELVEGLKELGIECTRSNGGFYCWADMRGLISSYSEKGEIELWNKLLNI
                     GKINVIPGSCCHCIEPGWFRICFSNLSERDVPVVMNRIRKVCETCKSQN"
BASE COUNT      473 a    354 c    410 g    520 t
ORIGIN

  Query Match           36.6%;  Score 147.8;  DB 8;  Length 1757;
  Best Local Similarity   63.8%;  Pred. No. 5.3e-36;
  Matches  256;  Conservative    0;  Mismatches  142;  Indels    3;  Gaps    2;

Qy       4 TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
           || | |||| | ||    |  | |||||||||| | ||||||||  ||  |  |  || |
Db    1230 TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 1289

Qy      64 AAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATG 123
           | |||| | ||||   | ||| |  | ||| |||| || || |  |||||  |
Db    1290 AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 1349

Qy     124 CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
            ||||  |  |          ||| |  ||  |  |    |||||   || | |  | ||
Db    1350 ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 1409

Qy     184 ATGTACGCTGCATTCGTGGCGGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
           || ||| | |   ||||||  |||||||||  |  | || |||   |||||   |||||
Db    1410 ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 1468

Qy     244 CGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAA 303
            |||||  |  |||| |||||||| || ||| | |||||||||  ||| ||||||||||||
Db    1469 TGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTGATTTCATCTTACAGCGAAAAA 1526

Qy     304 GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGT 363
           || ||| | ||||| ||| |||||  |  | |||||||  ||| | || || |  || ||
Db    1527 GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 1586

Qy     364 TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||||||||||| ||||| ||||| || |  ||  |  ||||
Db    1587 TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG 1627


RESULT 5
F16P17/c
LOCUS       F16P17                  98412 bp    DNA     linear   PLN 13-JUN-2000
DEFINITION  Sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1,
            complete sequence.
ACCESSION   AC011000
VERSION     AC011000.3  GI:7109456
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 98412)
  AUTHORS   Sakano,H., Liu,S.X., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi,M.,
            Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B.,
            Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q.,
            Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S.,
            Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
            Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
            Theologis,A.
  TITLE     The sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 98412)
  AUTHORS   Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-1999) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
REFERENCE   3  (bases 1 to 98412)
  AUTHORS   Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-FEB-2000) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
REFERENCE   4  (bases 1 to 98412)
  AUTHORS   Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2000) Plant Gene Expression Center, 800 Buchanan
            St., Albany, CA 94710, USA
COMMENT     On Feb 29, 2000 this sequence version replaced gi:6453846.
            The sequence is of BAC F16P17 from Arabidopsis thaliana chromosome
            1.  The sequence does not represent the sequence of the entire
            insert of this clone.  It is shorter by 10039 bp because we submit
            only the unique sequence of the clone.  However, in order to
            facilitate the joining of overlapping clones in the future, for
            creation of larger contigs, we provide small overlaps (200 bp)
            between overlapping sumbitted clones.  The 5' end of this sequence
            overlaps by 200 bp to the 3' end of the sequence of the clone
            F23N19.
FEATURES             Location/Qualifiers
     source          1. .98412
                     /organism="Arabidopsis thaliana"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="1"
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     gene            complement(1043. .2844)
                     /gene="F16P17.1"
     CDS             complement(join(1043. .1069,1256. .2068,2140. .2844))
                     /gene="F16P17.1"
                     /note="Contains multiple PPR Repeats PF|01535."
                     /codon_start=1
                     /evidence=not_experimental
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                     /translation="MVETGCPANVVTFTTLMNGLCREGRVLQALALVDRMVEEGHQPD
                     AVTYGTIVNGMCKLGDTVSALNMLRKMDESQIKANVVIYSAIVDRLCKDGNHIKAQNI
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                     VKEGKVSGAEELYREMLRRNIFPTTITYSSMIDGFCKHSRLEDAKHMFDLMVSKGCSP
                     DIITLNTLIDGCCRAKRHLIHGFCQVGNVNVAQDLFQEMISNGVSPDIVTCNTLLAGL
                     CENGKLEKALEMFKVFQKSKMDLDTATCNIIINGMCKGNKVDEAWDLFNSLPVNGVET
                     DVVTYNILIGVFVKEGNFLRAEDIYLEMLCKGIIPSTVTYNSMVDGFCKQNRLEEARQ
                     MVDSMVSEGCSPDVVTFSTLIKGYCKAGRVDDGLELFSEMCQRGLVADTITYNALIHG
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                     ELEDDE"
     gene            complement(10587. .12875)
                     /gene="F16P17.2"
     CDS             complement(10587. .12875)
                     /gene="F16P17.2"
                     /note="Contains weak similarity to T-type calcium channel
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                     comes from this gene."
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                     PLSVVDPSRFCGQFPVTQQPHLMLSGGKDDLGPLAMLEDSVKKLKSPKTSQTRNLTKA
                     QIDSALDSLSDWVFESCGSVSLSGLEHPKLRAFLTQVGLPIISRRDFVTGRLDLKYED
                     SRAEAESRIHDAMFFQIASDGWKFDSSGENLVNLIVNLPNGTSLYRRAVFVNGAVPSN
                     YAEEVLWETVRGICGNSPQRCVGIVSDRFMSKALRNLESQHQWMVNLSCQFQGFNSLI
                     RDFVKELPLFKSVSQSCSRLVNFVNSTAQIRNAVCKYQLQEQGETRMLHLPLDSSLFE
                     PLYNLLEDVLSFARAIQLVMHDDVCKAVLMEDHMAREVGEMVGDVGFWNEVEAVYLLL
                     KLVKEMARRIEEERPLVGQCLPLWDELRSKIKDWYAKFNVVEERQVEKIVERRFKKSY
                     HPAWAAAFILDPLYLIKDSSGKYLPPFKCLSPEQEKDVDKLITRLVSRDEAHIAMMEL
                     MKWRTEGLDPVYARAVQMKERDPVSGKMRIANPQSSRLVWETYLSEFRSLGRVAVRLI
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gene            18492. .19560
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                ER-derived vesicles from Saccharomyces cerevisiae
                gi|6321384.  ESTs gb|T22150, gb|AI100633, gb|AA395672 come
                from this gene."
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                /db_xref="GI:8493595"
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                DWEKKKRLFKLAYIILTLFLTIFW"
misc_feature    complement(22027. .23274)
                /note="Contains similarity to Limpet1_transposon."
gene            24159. .24903
                /gene="F16P17.4"
CDS             join(24159. .24411,24497. .24561,24604. .24903)
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                O-methyltransferase domain PF|00891."
                /codon_start=1
                /evidence=not_experimental
                /protein_id="AAF75800.1"
                /db_xref="GI:8493577"
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                IFMKWILHDWTDEDCVKILKNYWKSLPEKGKVIIVEVVTPEEPKINDISSNIVFGMDM
                LMLAVSSGGKERSLSQFETLASDSGFLRCEIICHAFSYSVIELHK"
gene            25427. .27325
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CDS             25427. .27325
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                ISLGEQMQTLGISHDLYTYSIFINCFCRRSQLSLALAVLAKMMKLGYEPDIVTLSSLL
                NGYCHSKRISDAVALVDQMVEMGYKPDTFTFTTLIHGLFLHNKASEAVALVDQMVQRG
                CQPDLVTYGTVVNGLCKRGDIDLALSLLKKMEKGKIEADVVIYNTIIDGLCKYKHMDD
                ALNLFTEMDNKGIRPDVFTYSSLISCLCNYGRWSDASRLLSDMIERKINPNVVTFSAL
                IDAFVKEGKLVEAEKLYDEMIKRSIDPDIFTYSSLINGFCMHDRLDEAKHMFELMISK
                DCFPNVVTYSTLIKGFCKAKRVEEGMELFREMSQRGLVGNTVTYTTLIHGFFQARDCD
                NAQMVFKQMVSVGVHPNILTYNILLDGLCKNGKLAKAMVVFEYLQRSTMEPDIYTYNI
                MIEGMCKAGKVEDGWELFCNLSLKGVSPNVIAYNTMISGFCRKGSKEEADSLLKKMKE
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gene            27943. .29529
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CDS             27943. .29529
                /gene="F16P17.6"
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                KMEILGISHNLYTYNILINCFCRCSRLSLALALLGKMMKLGYEPDIVTLNSLLNGFCH
                GNRISDAVALVDQMVEMGYKPDTVTFTTLIHGLFLHNKASEAVALIDRMVQRGCQPDL
                VTYGAVVNGLCKRGDTDLALNLLNKMEAAKIEANVVIYSTVIDSLCKYRHEDDALNLF
                TEMENKGVRPNVITYSSLISCLCNYGRWSDASRLLSDMIERKINPNLVTFSALIDAFV
                KKGKLVKAEKLYEEMIKRSIDPNIFTYSSLINGFCMLDRLGEAKQMLELMIRKDCLPN
                VVTYNTLINGFCKAKRVDKGMELFREMSQRGLVGNTVTYTTLIHGFFQARDCDNAQMV
                FKQMVSVGVHPNILTYNILLDGLCKNGKLAKAMVVFEYLQRSTMEPDIYTYNIMIEGM
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gene            32949. .34790
                /gene="F16P17.7"
CDS             32949. .34790
                /gene="F16P17.7"
                /note="Contains weak similarity to leaf protein from
                Ipomea nil gb|D85101 and contains a RepB PF|01051 protein
                and multiple PPR PF|01535 repeats."
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                /protein_id="AAF75803.1"
                /db_xref="GI:8493580"
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                FVMEYQPNTVTFNTLIHGLFLHNKASEAVALIDRMVARGCQPDLFTYGTVVNGLCKRG
                DIDLALSLLKKMEKGKIEADVVIYTTIIDALCNYKNVNDALNLFTEMDNKGIRPNVVT
                YNSLIRCLCNYGRWSDASRLLSDMIERKINPNVVTFSALIDAFVKEGKLVEAEKLYDE
                MIKRSIDPDIFTYSSLINGFCMHDRLDEAKHMFELMISKDCFPNVVTYNTLIKGFCKA
                KRVEEGMELFREMSQRGLVGNTVTYNTLIQGLFQAGDCDMAQKIFKKMVSDGVPPDII
                TYSILLDGLCKYGKLEKALVVFEYLQKSKMEPDIYTYNIMIEGMCKAGKVEDGWDLFC
                SLSLKGVKPNVIIYTTMISGFCRKGLKEEADALFREMKEDGTLPNSGTYNTLIRARLR
                DGDKAASAELIKEMRSCGFVGDASTISMVINMLHDGRLEKSYLEMLS"
gene            complement(35247. .35753)
                /gene="F16P17.8"
CDS             complement(35247. .35753)
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                /codon_start=1

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  Best Local Similarity   63.8%;  Pred. No. 9.5e-36;
  Matches  256;  Conservative    0;  Mismatches  142;  Indels    3;  Gaps    2;

Qy       4 TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
           || | |||| | ||     |  | |||||||||| | ||||||||  ||  |  |  || |
Db   45120 TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 45061

Qy      64 AAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATG 123
             | |||| | ||||   | ||| |  | ||| |||| || || |  |||||  |
Db   45060 AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 45001

Qy     124 CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
            ||||  |  |          ||| |  ||  |  |    |||||   || | |  | ||
Db   45000 ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 44941

Qy     184 ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
           || ||| | |   ||||||  |||||||||  |  | || |||   |||||   |||||
Db   44940 ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 44882

Qy     244 CGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAA 303
            |||||  |  |||| |||||||| || ||| | |||||||||  ||| ||||||||||||
Db   44881 TGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTGATTTCATCTTACAGCGAAAAA 44824

Qy     304 GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGT 363
           || ||| | ||||| ||| ||||| |  | |||||||  ||| | || || |  || ||
Db   44823 GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 44764

Qy     364 TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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Db   44763 TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG 44723


RESULT 6
TAU35779
LOCUS       TAU35779                1089 bp    mRNA    linear   PLN 07-NOV-1996
DEFINITION  Triticum aestivum 1-aminocyclopropane-1-carboxylate synthase (ACS1)
            mRNA, partial cds.
ACCESSION   U35779
VERSION     U35779.1  GI:1173637
KEYWORDS    .
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SOURCE      Triticum aestivum.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1089)
  AUTHORS   Subramaniam,K., Abbo,S. and Ueng,P.P.
  TITLE     Isolation of two differentially expressed wheat ACC synthase cDNAs
            and the characterization of one of their genes with
            root-predominant expression
  JOURNAL   Plant Mol. Biol. 31 (5), 1009-1020 (1996)
  MEDLINE   97000913
   PUBMED   8843943
REFERENCE   2  (bases 1 to 1089)
  AUTHORS   Subramaniam,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-1995) Kuppuswamy Subramaniam, USDA-ARS,
            Beltsville Agricultural Research Center, Plant Molecular Biology
            Laboratory, Beltsville, MD 20705, USA
FEATURES             Location/Qualifiers
     source          1. .1089
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                     /db_xref="taxon:4565"
                     /clone="pWAS-1"
     gene            1. .1089
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     CDS             1. .>1089
                     /gene="ACS1"
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                     NPSNPTGSFVPKQTLRDLLDFATEKNIHLISDEVFAGSTFGSGEFVSVAEVVNELEDF
                     DRGRVHIIYGLSKDLSLAGFRVGVIYSYNESIVEAAAKIARFSSVSTPTQRLLVAMLS
                     DQKFISNYLKVNRERLRKAYNLLVDALKQVGIECFKSSGGFYCWADMSKFIRSYSEKG
                     ERRLWDRLLEEAKVNVTPGSSCHCIEPGW"
BASE COUNT      274 a    248 c    303 g    264 t
ORIGIN

  Query Match             36.3%;  Score 146.8;  DB 8;  Length 1089;
  Best Local Similarity   64.8%;  Pred. No. 1e-35;
  Matches  249;  Conservative    0;  Mismatches  132;  Indels    3;  Gaps    2;

Qy       8 CGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCAAAA 67
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Db     707 CAGGGTTTCGAGTCGGAGTCATATATTCGTATAACGAAAGCATTGTGGAGGCAGCCGCCA 766

Qy      68 AGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCT 127
           || |  | ||||| |||||  | ||  | ||||| |||||| | || || |  |||||
Db     767 AGATTGCCAGATTCTCATCTGTGTCGACCCCGACCCAGCGCCTTCTTGTTGCCATGCTTT 826

Qy     128 CGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGT 187
           |||||  |  ||| | |  ||| | | |  | || ||||||| ||  ||    |    ||
Db     827 CGGACCAGAAGTTTATTTCAAATTACCTGAAAGTTAACAGAGAGAGGCTGCGCAAGGCGT 886

Qy     188 ACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGA 247
           ||  |    |||| |   |  |||||| |  | ||||||   |||    | |||||||||
Db     887 ACAATCTGCTCGTTG-ATGCTTTGAAGCAGGTGGGCATCGAGTGCTTCAAGAGCAGCGGA 945

Qy     248 GGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAG 307
           || |  |||| || ||||| |||||||||   || || || || |||||||| |||||||
Db     946 GGGT--TCTACTGCTGGGCAGACATGAGCAAGTTCATCCGGTCTTACAGCGAGAAAGGAG 1003

Qy     308 AGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTT 367
           ||| |  ||| ||||||| | || |  |    || ||||| || || || || ||||| |
Db    1004 AGCGCAGGCTTTGGGACAGGCTGTTGGAGGAGGCGAAGGTCAATGTCACCCCAGGTTCAT 1063

Qy     368 GTTGTCATTGTATTGAACCCGGCT 391
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Db    1064 CTTGCCATTGCATTGAGCCGGGTT 1087


RESULT 7
AP000559
LOCUS       AP000559              143113 bp    DNA     linear   PLN 21-MAR-2002
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
            clone:P0493C11.
ACCESSION   AP000559
VERSION     AP000559.1  GI:6006355
KEYWORDS    .
SOURCE      Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
            clone:P0493C11.
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
            clone:P0493C11
  JOURNAL   Published Only in Database (1999)
REFERENCE   2  (bases 1 to 143113)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-1999) Takuji Sasaki, National Institute of
            Agrobiological Resources, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     The orientation of the sequence is from T7 to SP6 of the PAC clone.
            Genes were predicted from the integrated results of the
            following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as
            SplicePredictor (October1998 version). The genomic sequence was
            searched against the non-redundant database NRP(PIR,SWISSPROT,
            GENPEPT, PDB) from MAFF DNAbank and the cDNA sequence database at
            RGP. Protein similarities of the cording regions were searched
            against NRP with BLASTP2.0. ESTs represent the identified cDNA
            sequences using BLASTN2.0 with the corresponding DDBJ accession no.
            and RGP clone ID.
FEATURES             Location/Qualifiers
     source          1. .143113
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                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /chromosome="6"
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     CDS             join(40. .126,585. .819,1979. .2001,2924. .2946,3836. .4073)
                     /note="hypothetical protein"
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                     /db_xref="GI:6006356"
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                     FLAARKREPNQEQHGSSNGVPWMALQIDLHNGSSNLLTSPE"
     CDS             join(7961. .8199,8666. .8737,8962. .9033,9134. .9205,
                     9487. .9558,9770. .9841,9939. .10010,10098. .10169,
                     10254. .10322,10440. .10511,10637. .10708,10792. .10863,
                     10948. .11019,11102. .11173,11262. .11333,11448. .11519,
                     11611. .11682,11795. .11866,11963. .12034,12124. .12195,
                     12272. .12353,12398. .12515,12601. .12732,12838. .13176,
                     13259. .13629,13761. .14114)
                     /note="ESTs C22657(S0014),C22656(S0014) correspond to a
                     region of the predicted gene.
                     Similar to receptor protein kinase, ERECTA (AC004484)"
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                     /protein_id="BAA84787.1"
                     /db_xref="GI:6006357"
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GPIPSTLSQIPNLKTLDLAQNQLTGDIPRLIYWNEVLQYLGLRGNSLTGTLSPDMCQL
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VYGNKLNGSIPAGFQKLESLTYLNLSSNNFKGNIPSELGHIINLDTLDLSYNEFSGPV
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CDS complement(join(14588. .14693,15191. .15299,15896. .15968,
16609. .16683,16765. .16827,17295. .17364,17675. .17845,
18666. .18766,19737. .19845,20254. .20410,20534. .20683,
21424. .21542,21971. .22225,22674. .23145,23660. .23750))
/note="Similar to Arabidopsis thaliana DNA chromosome 4,
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LMKPTASQLARQNRQIEVKNSTQSKKSVGVRSDRSTMSSNDCTYQAAKRQRLERGHLN
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PSGRNDHQHASVPHRGIGSNVPVCTANRPRHLDNICKTPDECRDDLFKFKARPVDKKE
FKLSTGRKGKQAPLSELFNKLTLTTEARRALDHRTADLPNYITTKLNIIPYLLAAMAE
IDLYRETNHDAGVHSPVQFLLEPVTDSTSFDENQSKTTEFRGSNAGRKHSNEPTKQDI
NTRHGDSEFQRQQQQQQQQTDVH"

CDS join(24594. .24979,25296. .25323,25853. .26051,26163. .26335,
26839. .26934,27845. .28007,28363. .28482,29210. .29521,
30922. .31079)
/note="hypothetical protein"
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/protein_id="BAA84789.1"
/db_xref="GI:6006359"
/translation="MHAVNATQRARHACRRRAVSVQQQREIERATKGRPRPRRRRRRR
WWMARGEVVCSCPWFLSLKPLVTSAAASTKRRRRRLGGVAVVVELGWSEIQRPRDWPL
CFGSEVMGQKDIAGLDLHNAFVCLKPTYLQSPFYLRKFYHQLTYQYNKRLLVKSELLC
RFGGKLDNDNTVAKSKPYMLFLSSLVTTTLRWVPLVVSVANELWLLKKKQAAAGSSRA
RAPPLATRQSLAVPLFPGTAARCCCCCSCAERLWTMPLGVDEEELYRNTSLLENIILQ
VEFGGFNIAESGKAEENRYYMVAPVAGDRTDPAGFCSTDGMCDALCYSGICTVWFWSS
PHACRPIAFTVSKWGLTRAVRERDGHVANVQLDAHCVVRPRCNRVSTDNSPGRTGLCF
YCDCGQSDNCVPPESPTAAGTVLLHVFYLYQSTTIFVVGHRKQPTVQSHCVTQILSGE
SHKIKRVCPMLGLFRSVGTGLFANREYFSCFPLQNSDISANRGLQFANYKQASRTTRK
SYPNHDDHQLRVKCIFFCYAYSMPWQQRRYVEEITR"

CDS join(32052. .32510,32612. .32761,34106. .34266,34349. .35207)
/note="Similar to 1-aminocyclopropane-1-carboxylate
synthase (U35779)"
/codon_start=1
/protein_id="BAA84790.1"
/db_xref="GI:6006360"
/translation="MRRSGNGGAAKKKKKRSASAASERRPRADGGMRIVVPLQGVVQG
RGGLVLGSLIPCALFYFFQLYIKRNRASPPPPPGSPTAASAAAVSPIHRSLSRGLLAP
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RWMEEHAAEAASMAGGEDEDERELSIRGLAAYQPYDGILALKMALAGFMRQIMQGSVS
FEPSQVVITSGATPAMEILSFCLADPGNAFLVPSPYYPGWDRDIKWRTGIELIPVPCR
STDNFNISITALEIAYNQAKKRGIKVRGVLISNPNNPTGSFVPKQTLHDLLEFAAEKN
IHLISDEVFAGSTYGSGKFVSVAEVVDDLEDFDKGRVHIIYGLSKDLSLAGFRVGVIY
SYNESIVTAAAKIARFSSVSTPTQRLLVAMLSDQKFISDYLKVNRERLRKMYHLFVDA
LDQVGIECYKSSGGFYCWADMSKFIRSYSEKGERKLWDRLLEEAKVNVTPGSSCHCIE
PGWFRCCFTTLSEHDIPVLVQRLRTITDSHKPNH"

CDS join(37342. .37344,37434. .37913)
/note="ESTs AU030008(E50477),AU078239(E50477) correspond
to a region of the predicted gene.
Similar to peptidyl-prolyl cis-trans isomerase 10
&CELB0252_4 (P52017)"
/codon_start=1
/protein_id="BAA84791.1"
/db_xref="GI:6006361"
/translation="MSVTLHTNLGDIKCEVFCDQAPRTAENFLALCASGYYDGTIFHR
NIKGFMIQGGDPTGTGKGGTSIWGKKFADEFRESLKHNARGVMSMANSGPNTNGSQFF
ITYAKQPHLNGHYTVFAKVIHGFEVLDLMEKAQTGPGDRPLAEIRLNRVTIHANPLAN
"

CDS complement(join(39025. .39194,39720. .39888))
/note="Similar to Arabidopsis thaliana chromosome II BAC
T32F12, hypothetical protein (AC005314)"
/codon_start=1
/protein_id="BAA84792.1"
/db_xref="GI:6006362"
/translation="MNDRDNAIRERDHALAEKKAAIAERDMAFTQRDAAMAERNAAVV
ERDNALAALELALMPNKRHARMGGRKMSGGAFTKLLSRLAAEGHDLSTPVDLKDHWAK
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CDS complement(join(45085. .45552,45642. .45896))
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a region of the predicted gene.
Similar to water stress inducible protein (U74296)"
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KAARSKAAKGVVGGAKRKRTPRPSAAAAKKPASSAEAKKAVPPARPARAKRARKAAPA
KPMQPPKSIRSAISKKANKASA"

CDS complement(join(47867. .48205,48314. .48385))
/note="EST D15300(C0425) corresponds to a region of the
predicted gene.
Similar to histone H3 (AB015760)"
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/db_xref="GI:6006364"
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CDS complement(join(49556. .50196,50838. .51051))
/note="hypothetical protein"
/codon_start=1
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/db_xref="GI:6006365"
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MSGREGWKQTSLTAARWPRSTATGSGAAGGAAHRCIGWATPGVDDRQRLEQASGKKGA
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PPGPPPPLALSPLLSHRTLATPTFGDNVDDNGGVVSIARGGVKRDDFTVLGSPPRAVV
EEATMEMRSTTVSEGGARIEMRSTIVTEGNARIEMCRAPLLFCRPPAACHSNPAVPPL
ATPLPRRG"

CDS join(59800. .59950,61242. .61397,61635. .61777,62523. .62570)
/note="hypothetical protein"
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/protein_id="BAA84796.1"
/db_xref="GI:6006366"
/translation="MLPAATAAVTVSAIDVGDGEERPLCRNGSSCDGPTATHRPWWPW
CQWPSESLSIGSGLAFDVSTGTVCSNAYSNKGQFLDQALFHLFGWAEIPALCWEKKHQ
VPGNDRKEYVLFRGARQWWYRGEVKKGGVLVAAASRSRFSVYYYFSVQRTTGGKRWRA
MSGIT"

Query Match 35.7%; Score 144.2; DB 8; Length 143113;
Best Local Similarity 63.9%; Pred. No. 1.4e-34;
Matches 250; Conservative 0; Mismatches 138; Indels 3; Gaps 2;

Qy 8 CGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCAAAA 67
Db 34729 CCGGGTTTCGGGTTGGGGTAATATATTCCTATAATGAAAGCATCGTGACAGCAGCTGCTA 34788

Qy 68 AGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCT 127
Db 34789 AGATTGCTAGGTTCTCGTCTGTGTCAACTCCAACACAACGCTTGCTTGTTGCCATGCTCT 34848

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Qy    128 CGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGT 187
          |||||     |||||  |   | | | | |   | || || |||| || | |     |  ||||
Db  34849 CGGACCAAAAGTTCATTTCAGATTACCTAAAAGTTAATAGAGAGAGATTGCGCAAGATGT 34908

Qy    188 ACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGA 247
          ||  |   || || |    |  ||| |  || | || ||    |||    | |||||  |||
Db  34909 ACCATTTGTTTGTTG-ATGCTTTGGATCAAGTGGGGATTGAGTGCTACAAGAGCAGTGGA 34967

Qy    248 GGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAG 307
          || |  |||| || ||||| |||||||||   || ||  | || |||||||| ||||| |
Db  34968 GGGT--TCTACTGCTGGGCAGACATGAGCAAGTTCATCAGGTCTTACAGCGAGAAAGGGG 35025

Qy    308 AGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTT 367
          ||| | |||| ||||| | |||  |  |    || ||||| || || ||||| ||||| |
Db  35026 AGCGCAAGCTTTGGGATAGGTTATTGGAGGAGGCAAAGGTCAATGTCACTCCAGGTTCAT 35085

Qy    368 GTTGTCATTGTATTGAACCCGGCTACTTTAG 398
           ||| ||||| || || || || |  || ||
Db  35086 CTTGCCATTGCATCGAGCCTGGATGGTTCAG 35116
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RESULT 8
AF336920

```
LOCUS       AF336920               1488 bp    mRNA    linear   PLN 18-APR-2002
DEFINITION  Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase
            ACS12 (At5g51690) mRNA, complete cds.
ACCESSION   AF336920
VERSION     AF336920.1  GI:12484204
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1488)
  AUTHORS   Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,
            Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,
            Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
            Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
            Theologis,A.
  TITLE     Arabidopsis Open Reading Frame (ORF) Clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1488)
  AUTHORS   Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
            Goldsmith,A.D., Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q.,
            Chen,H., Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
            Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
            Theologis,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
FEATURES             Location/Qualifiers
     source          1. .1488
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
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                     /clone="C00056"
                     /note="This clone is in pUNI-T3-D/V5-His-TOPO.
                     ecotype: Columbia"
     gene            1. .1488
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                     /evidence=experimental
     CDS             1. .1488
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                     /protein_id="AAG54001.1"
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                     FADFMSRIMGGNVSFDPSNMVITAGGTPAIEVLAFCLADHGNAFLIPTPYYPGFDRDI
                     KFRTGVELIPVHCRSSDNFTVTVSALEQALNQARKRGSKVSGILFSNPSNPVGNILSR
                     ETLCDILRFAQEKNIHVISDEIFAGSVYGDKEFVSMAEIAGSGEFDKTRVHIIYGLSK
                     DLSIPGFRAGVIYSFHEDVVNAAKKLMRFSSVPVLVQRILISLLSDVRFIEGYMAAHR
                     QRIRDKHIRFVEGLKQLGIPCAESGGGLYCWVDMSSLLTSYSEKGELELFEKLLTVAK
                     INATPGTACYCIEPGWFRCCFTALADEDIPVIMERIRQLAESFRS"
BASE COUNT      386 a    289 c    359 g    454 t
ORIGIN
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  Query Match             31.6%;  Score 127.6;  DB 8;  Length 1488;
  Best Local Similarity   60.8%;  Pred. No. 1.6e-29;
  Matches  243;  Conservative    0;  Mismatches  154;  Indels    3;  Gaps    2;

Qy      5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
          | || || || ||    || || ||||||||||   | ||  ||||  | | | |||| |
Db   1013 TTCCTGGTTTTAGAGCTGGAGTCATCTACTCCTTTCATGAAGACGTAGTAAATGCTGCAA 1072

Qy     65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
          | ||| ||| ||||||||||||  |  ||| ||     ||  |  | ||  ||  | | |
Db   1073 AGAAGCTGATGAGATTTTCATCAGTGCCAGTTCTAGTTCAAAGGATACTTATCTCTCTAC 1132

Qy    125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
          | || ||     | |||| | |    | ||| |  | | ||||    |   ||      |
Db   1133 TATCTGATGTAAGATTCATTGAGGGATACATGGCAGCACACAGGCAAAGGATCCGGGATA 1192

Qy    185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
          | |   |   || ||||   || |||||  || | || || | |||  | || ||  |
Db   1193 AGCATATTCGGTTTGTGG-AAGGTTTGAAACAATTAGGAATACCATGTGCTGAGAGTGGT 1251

Qy    245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
          || || |  | ||||||||||  |||||||||| | ||  |   ||| ||||| || ||||
Db   1252 GGTGGGT--TGTATTGTTGGGTAGACATGAGCAGTTTACTGACATCTTACAGTGAGAAAG 1309

Qy    305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
          |||| ||||||| |||  || ||| |  | |   |||||||| | || |  ||||| ||
Db   1310 GAGAACTCGAGTTATTTGAGAAGCTATTGACTGTTGCTAAGATTAATGCCACTCCAGGAA 1369

Qy    365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          |    ||| ||||||| ||||| || |  || ||   |||
Db   1370 CAGCCTGTTATTGTATAGAACCAGGTTGGTTCAGGTGCTG 1409
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RESULT 9
AB010074/c

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LOCUS       AB010074               86212 bp    DNA     linear   PLN 27-DEC-2000
DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIO24.
ACCESSION   AB010074 BA000015
VERSION     AB010074.2  GI:10177866
KEYWORDS    .
SOURCE      Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
            clone:MIO24.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Sato,S., Kaneko,T., Kotani,H., Nakamura,Y., Asamizu,E., Miyajima,N.
            and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 5. IV.
            Sequence features of the regions of 1,456,315 bp covered by
            nineteen physically assigned P1 and TAC clones
  JOURNAL   DNA Res. 5 (1), 41-54 (1998)
  MEDLINE   98290546
REFERENCE   2  (bases 1 to 86212)
  AUTHORS   Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     On Sep 15, 2000 this sequence version replaced gi:2760170.
            Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
```

```
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MIO24
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zcol.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is K10D11 and the 3' clone is MJM18.
FEATURES            Location/Qualifiers
     source         1. .86212
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                    /strain="Columbia"
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                    /clone_lib="Mitsui P1"
     CDS            1494. .2471
                    /note="gene_id:MIO24.19
                    unknown protein"
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                    /evidence=not_experimental
                    /protein_id="BAB11237.1"
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                    ASSDSFSSVPSLLATNRSVSISGAVAVDEFDDNLNTVTSSMPTSPAYESDDSTSSYMT
                    GASSLVGASFLEKLFPRLLPSEKVKAAVSEDVQVSTHPLHEEVKLTTETDNMSIGFPV
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                    /protein_id="BAB11238.1"
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                    IMGGNVSFDPSNMVITAGGTPAIEVLAFCLADHGNAFLIPTPYYPGFDRDIKFRTGVE
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     CDS            complement(join(8613. .8741,8843. .8887,8984. .9061,
                    9159. .9303,9399. .9538,9772. .9825,9931. .10027,10121. .10209,
                    10297. .10374,10479. .10547,10630. .10713,10811. .10882,
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                    LELGSFVAGVMLSTTEFAQHTLEQVLILNSGRFCFASTCIGMLINVHFLWNHVDILLA
                    SVILVIVIKTAIAAVVVKAFRYNMRISFHVGVLLAQIGEFAFVLLSRASNLHVIEGKM
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                    LLLKKQ"
     CDS            join(15321. .15363,15628. .15683,15772. .15942,16064. .16144,
                    16336. .16371,16445. .16623,16711. .16860,16938. .17116,
                    17217. .17560)
                    /note="gb|AAF69708.1
                    gene_id:MIO24.15
                    similar to unknown protein"
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                    /evidence=not_experimental
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                    VRPVIQNSASSEDLKISDQGEEPAHKKAKTDTNTCKKESSRNVSSKESDVVKKETLER
                    TLPTYSFKNLTKTAEVGERALFIPKQGGRYDCGTIFVKGYDSSLGENDLARALLEHFS
                    PCGMISRIYFQTNDAGEAVLKHVFIVMLQGTEDALKLNGSDMGGCNLEVHDATERDEF
                    YVNYEVSGGPFIKKPCQRLLARQKIPLCMALSVLARSTSNSDQPQALNLSESEAYNRP
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                    /translation="MKPSLKRRLLLLSRKFAKASIRKLLRQSSFSSHEFLLQAPFPAM
                    SWYRRTKLVFDSLRRNINPKILPRSHVTSRINNPIGSSNPSAKFSSISSREVGLRSWT
                    SLGRNTNRIAYNPFLSQPKRYYYVDRYQVRHFKPRGPGRWFQNPRTVFTVVLVGSVGL
                    ITLIVGNTETIPYTKRTHFILLSKPMEKLLGETQFEQIKKTYQGKILPATHPESIRVR
                    LIAKEVIDALQRGLSNERVWSDLGYASTESSLGGGSDKGVKEMEMAMSGEDTMTDMKW
                    SKEDQVLDDQWIQKSRKKDSKAHAATSHLEGISWEVLVVNEPIVNAFCLPAGKIVVFT
                    GLLNHFKSDAEVATVIGHEVGHAVARHVAEGITKNLWFAILQLVLYQFVMPDLVNTMS
                    ALFLRLPFSRKMEIEADYIGLLLASAGYDPRVAPTVYEKLGKLGGDALGDYLSTHPS
                    GKKRSKLLAQANVMEEALMIYREVQAGRTGVEGFL"
     CDS            24169. .26511
                    /note="gene_id:MIO24.12"
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                    /evidence=not_experimental
                    /product="serine protease-like protein"
                    /protein_id="BAB11244.1"
                    /db_xref="GI:10177874"
                    /translation="MANKNPLQKPFLFIILSINLIFLQAETTTQISTKKTYVIHMDKS
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                     SESFNDTGMSPVPATWRGACETGKRFLKRNCNRKIVGARVFYRGYEAATGKIDEELEY
                     KSPRDRDGHGTHTAATVAGSPVKGANLFGFAYGTARGMAQKARVAAYKVCWVGGCFSS
                     DILSAVDQAVADGVQVLSISLGGGVSTYSRDSLSIATFGAMEMGVFVSCSAGNGGPDP
                     ISLTNVSPWITTVGASTMDRDFPATVKIGTMRTFKGVSLYKGRTVLPKNKQYPLVYLG
                     RNASSPDPTSFCLDGALDRRHVAGKIVICDRGVTPRVQKGQVVKRAGGIGMVLTNTAT
                     NGEELVADSHMLPAVAVGEKEGKLIKQYAMTSKKATASLEILGTRIGIKPSPVVAAFS
                     SRGPNFLSLEILKPDLLAPGVNILAAWTGDMAPSSLSSDPRRVKFNILSGTSMSCPHV
                     SGVAALIKSRHPDWSPAAIKSALMTTAYVHDNMFKPLTDASGAAPSSPYDHGAGHIDP
                     LRATDPGLVYDIGPQEYFEFLCTQDLSPSQLKVFTKHSNRTCKHTLAKNPGNLNYPAI
                     SALFPENTHVKAMTLRRTVTNVGPHISSYKVSVSPFKGASVTVQPKTLNFTSKHQKLS
                     YTVTFRTRFRMKRPEFGGLVWKSTTHKVRSPVIITWLPPL"
     CDS             join(30819. .31283,31350. .31694,31761. .31866,32481. .32815)
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                     /codon_start=1
                     /evidence=not_experimental
                     /product="protein phosphatase-2C; PP2C-like protein"
                     /protein_id="BAB11245.1"
                     /db_xref="GI:10177875"
                     /translation="MTEIYRTISTGRGDDVSPTKCRERRRRRIEMRRQAAVFGEPSSS
                     RNRDRTDMEVYSSFDVPLRKQARRSEIGGLPADIGGFLAPPAASSCQKSEAPVWKGEE
                     TEDEPLYGIVSVMGRSRKMEDSVTVKPNLCKPEVNRQRPVHFFAVYDGHGGSQVSTLC
                     STTMHTFVKEELEQNLEEEEEGSENDVVERKWRGVMKRSFKRMDEMATSTCVCGTSVP
                     LCNCDPREAAISGSTAVTAVLTHDHIIVANTGDSRAVLCRNGMAIPLSNDHKPDRPDE
                     RARIEAAGGRVLVVDGARVEGILATSRAIGDRYLKPMVAWEPEVTFMRRESGDECLVL
                     ASDGLWDVLSSQLACDIARFCLREETPSSLDLNRMAQEDDNDGEQNPSRSVLAATLLT

  Query Match             31.6%;  Score 127.6;  DB 8;  Length 86212;
  Best Local Similarity   60.8%;  Pred. No. 2.8e-29;
  Matches  243;  Conservative    0;  Mismatches  154;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
           | || || || ||    || || ||||||||||   | ||  ||||  | | | |||| |
Db    3393 TTCCTGGTTTTAGAGCTGGAGTCATCTACTCCTTTCATGAAGACGTAGTAAATGCTGCAA 3334

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           | ||| ||| ||||||||||||  |  ||| ||     ||  |  | ||  ||  | | |
Db    3333 AGAAGCTGATGAGATTTTCATCAGTGCCAGTTCTAGTTCAAAGGATACTTATCTCTCTAC 3274

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | ||  ||     | ||||  | |    | ||| |  | | ||||    |   ||      |
Db    3273 TATCTGATGTAAGATTCATTGAGGGATACATGGCAGCACACAGGCAAAGGATCCGGGATA 3214

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
           | |   |   || ||||   || |||||  || | || || | |||  | || ||  |
Db    3213 AGCATATTCGGTTTGTGG-AAGGTTTGAAACAATTAGGAATACCATGTGCTGAGAGTGGT 3155

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
           || || |  | ||||||||||  |||||||||| | ||  |   ||| ||||| || ||||
Db    3154 GGTGGGT--TGTATTGTTGGGTAGACATGAGCAGTTTACTGACATCTTACAGTGAGAAAG 3097

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
           |||| |||||| |||  || ||| |  | |   |||||||| | || |  ||||| ||
Db    3096 GAGAACTCGAGTTATTTGAGAAGCTATTGACTGTTGCTAAGATTAATGCCACTCCAGGAA 3037

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           |    ||| ||||||| ||||| || |  || ||   |||
Db    3036 CAGCCTGTTATTGTATAGAACCAGGTTGGTTCAGGTGCTG 2997


RESULT 10
MSBACS2GE
LOCUS       MSBACS2GE               1372 bp    DNA     linear   PLN 01-MAR-2002
DEFINITION  Musa acuminata bacs2 gene for 1-aminocyclopropane-1-carboxylate
            synthase.
ACCESSION   X96947
VERSION     X96947.1  GI:1255948
KEYWORDS    1-aminocyclopropane-1-carboxylate synthase; bacs2 gene.
SOURCE      Musa acuminata.
  ORGANISM  Musa acuminata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
            Musa.
REFERENCE   1
  AUTHORS   Liu,J. and Pua,E.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1372)
  AUTHORS   Liu,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-1996) J. Liu, Department of Botany, National
            University of Singapore, Lower Kent Ridge Road, Singapore 119260,
            REPUBLIC OF SINGAPORE
FEATURES             Location/Qualifiers
     source          1. .1372
                     /organism="Musa acuminata"
                     /cultivar="AAA group, cavendish"
                     /db_xref="taxon:4641"
     gene            1. .1372
                     /gene="bacs2"
     mRNA            join(<1. .21,110. .241,327. .487,589. .>1372)
                     /gene="bacs2"
                     /product="1-aminocyclopropane-1-carboxylate synthase"
     CDS             join(1. .21,110. .241,327. .487,589. .>1372)
                     /gene="bacs2"
                     /EC_number="4.4.1.14"
                     /codon_start=1
                     /product="1-aminocyclopropane-1-carboxylate synthase"
                     /protein_id="CAA65648.1"
                     /db_xref="GI:1255949"
                     /db_xref="SPTREMBL:Q42924"
                     /translation="MGLAENQLSLDLIEGGLERHPDAVGLRRDGALVSRELALFQDYH
                     GLPASKKALADFMGELRGNKVKFEPHKLVLTAGSTSANETLMFCLAEPGEAFLLPTPY
                     YPGFDRDLKRRTGAEIVPIHCSSPNGFRVTKAALEKAYQGARKRHLRVKGVLVTNPSN
                     PLGTTMTRCELDTLMTFVVAKDIHLISDEICSGTSFDAPGFVSVMEAIEGRQHVSHRI
                     HVVYSLSKDLGLPGFRVGAIYSNNEAVVAAATKMSSFGLVSSQTQYLLSVLLSDKEFT
                     RNYIAENQKRIKERHDRLVQGLRRSGISCLQSNAGLFCWVDMRHLLNSNTFEGEMELW
                     KKIVYQVGLNISPGSSCHSHEPGWFRVCFANM"
     exon            <1. .21
                     /gene="bacs2"
                     /number=1
     intron          22. .109
                     /gene="bacs2"
                     /number=1
     exon            110. .241
                     /gene="bacs2"
                     /number=2
     intron          242. .326
                     /gene="bacs2"
                     /number=2
     exon            327. .487
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                     /number=3
     intron          488. .588
                     /gene="bacs2"
                     /number=3
     exon            589. .>1372
                     /gene="bacs2"
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BASE COUNT      284 a    411 c    364 g    313 t
ORIGIN

  Query Match             29.0%;  Score 117.2;  DB 8;  Length 1372;
  Best Local Similarity   58.9%;  Pred. No. 3.4e-26;
  Matches  238;  Conservative    0;  Mismatches  163;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || ||| || |||| |  |||||||| ||||||||   ||  |  |  |
Db     959 GGCCTCCCTGGCTTCCGGGTGGGTGCAATCTACTCCAACAACGAGGCAGTAGTGGCCGCC 1018

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || |  ||| || |||| |||  |  | | ||  | | ||| |||  | | |||   |||
Db    1019 GCTACCAAGATGTCGAGCTTTGGACTCGTCTCCTCCCAGACTCAGTACCTCCTCTCGGTT 1078

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
            |||||| |||| |  ||||||   ||| | ||| | ||  |||     ||   ||||
Db    1079 CTGCTCTCCGACAAGGAGTTCACCAGAAACTACATTGCGGAGAACCAGAAGAGGATCAAG 1138
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Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           .| |||      ||||  |  ||| |   || |  ||||||| | |||  | | ||
Db    1139 GAGCGGCACGACCGGCTCGT-CCAAGGGCTCCGGAGAAGCGGCATCAGCTGCCTGCAGAG 1197

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           || || |||  ||| |  || ||||  |||||||      || |    ||| |||
Db    1198 CAACGCAGG--TCTGTTCTGCTGGGTGGACATGAGGCACCTGCTGAACTCCAACACGTTC 1255

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |||||||| | ||||| ||| | ||| |  |  ||   |    | | ||| |  | ||
Db    1256 GAAGGAGAGATGGAGCTGTGGAAGAAGATCGTGTACCAAGTGGGGCTCAACATCTCGCCG 1315

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || |  || || |     || || || |  ||| || ||||
Db    1316 GGCTCCTCCTGCCACTCCCACGAGCCTGGGTGGTTTCGCGTCTG 1359


RESULT 11
MSBACS1GE
LOCUS       MSBACS1GE               1812 bp    DNA     linear   PLN 18-APR-1997
DEFINITION  M.acuminata bacs1 gene.
ACCESSION   X96946
VERSION     X96946.1  GI:1945274
KEYWORDS    1-aminocyclopropane-1-carboxylate synthase; bacs1 gene.
SOURCE      Musa acuminata.
  ORGANISM  Musa acuminata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
            Musa.
REFERENCE   1  (bases 1 to 1812)
  AUTHORS   Liu,J. and Pua,E.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1812)
  AUTHORS   Liu,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-1996) J. Liu, Department of Botany, National
            University of Singapore, Lower Kent Ridge Road, Singapore 119260,
            REPUBLIC OF SINGAPORE
  REMARK    revised by [3]
REFERENCE   3  (bases 1 to 1812)
  AUTHORS   Liu,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-1997) J. Liu, Department of Botany, National
            University of Singapore, Lower Kent Ridge Road, Singapore 119260,
            REPUBLIC OF SINGAPORE
COMMENT     On Apr 19, 1997 this sequence version replaced gi:1255946.
FEATURES             Location/Qualifiers
     source          1. .1812
                     /organism="Musa acuminata"
                     /cultivar="AAA group, cavendish"
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                     /clone_lib="pBluescript KS"
     gene            join(308. .460,551. .682,767. .927,1029. .1812)
                     /gene="bacs1"
     CDS             join(308. .460,551. .682,767. .927,1029. .>1812)
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                     /EC_number="4.4.1.14"
                     /codon_start=1
                     /product="1-aminocyclopropane-1-carboxylate synthase"
                     /protein_id="CAA65647.1"
                     /db_xref="GI:1945275"
                     /db_xref="SPTREMBL:Q42923"
                     /translation="MPQMLLSRKAACNTHGQDSSYFLGWQEYEKNPYDPRTNPTGIIQ
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                     GLRGDKVKFEPHKLVLTAGSTSANETLMFCLAEAGEAFPSPTPYYPGFDRDLKWRTGA
                     EIVPIHCSSSNGFRVTKAALEKAYQGPRKRHLRVKGVLVTNPSNPLGTAMTRCELDTL
                     IDFVVAKDIHLISDEIYSGTSFDAPRFVSVMEAIEGGQHVSHRIHVVYSLSKDLGLPG
                     FRVGAIYSNNGAVVAAATKMSSFGLVSSQTQYLLSVLLSDKEFTRNYHFENQKRIKER
                     HDRLVQGLRRSGISCLQSNAGLFCWVDMRHLLNSDTFKGEMELWRKIVYQVGLNISPG
                     SSCHCDEPGWFSVCFANM"
     intron          461. .550
                     /gene="bacs1"
                     /number=1
     intron          683. .776
                     /gene="bacs1"
                     /number=2
     intron          928. .1028
                     /gene="bacs1"
                     /number=3
BASE COUNT      405 a    518 c    456 g    433 t
ORIGIN

  Query Match             28.2%;  Score 114;  DB 8;  Length 1812;
  Best Local Similarity   58.4%;  Pred. No. 3.8e-25;
  Matches  236;  Conservative    0;  Mismatches  165;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || ||| || |||| |  |||||||  ||||||  |   ||  |  |  |
Db    1399 GGCCTCCCTGGCTTCCGGGTGGGTGCAATCTACTCAAACAACGGGGCAGTAGTGGCCGCC 1458

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || |  ||| || |||| |||  |  | | ||  | | ||| |||  | | |||   |||
Db    1459 GCTACCAAGATGTCGAGCTTTGGACTCGTCTCCTCCCAGACTCAGTACCTCCTCTCGGTT 1518

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           |||||||  |||| |  ||||||   ||| | |      |  |||     ||   ||||
Db    1519 CTGCTCTCCGACAAGGAGTTCACCAGAAACTACCATTTCGAGAACCAGAAGAGGATCAAG 1578

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           | | |||      ||||  |  ||| |   || |  ||||||| | |||  | | ||
Db    1579 GAGAGGCACGACCGGCTCGT-CCAAGGGCTCCGGAGAAGCGGCATCAGCTGCCTGCAGAG 1637

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           || || |||  ||| |  || ||||  |||||||     || |    ||| ||| |
Db    1638 CAACGCAGG--TCTGTTCTGCTGGGTGGACATGAGGCACCTGCTGAACTCCGACACCTTC 1695

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |||||||| | ||||| |||   ||| |  |  |     |      ||||| |  | ||
Db    1696 AAAGGAGAGATGGAGCTGTGGAGGAAGATAGTGTATCAAGTGGGACTAAACATCTCGCCG 1755

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || ||||  || || ||    ||||| || |  || ||| ||||
Db    1756 GGCTCTTCGTGCCACTGCGACGAACCGGGGTGGTTCAGCGTCTG 1799


RESULT 12
AF312737
LOCUS       AF312737                1400 bp    mRNA    linear   PLN 01-NOV-2000
DEFINITION  Malus x domestica ACC synthase mRNA, partial cds.
ACCESSION   AF312737
VERSION     AF312737.1  GI:11066995
KEYWORDS    .
SOURCE      Malus x domestica.
  ORGANISM  Malus x domestica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE   1  (bases 1 to 1400)
  AUTHORS   Trivedi,P.K. and Solomos,T.
  TITLE     An apple (Malus domestica L. Borkh cv Granny Smith) ACC synthase
            partial cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1400)
  AUTHORS   Trivedi,P.K. and Solomos,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-OCT-2000) NRSL, University of Maryland, Plant Science
            Building, College Park, MD 20742, USA
FEATURES             Location/Qualifiers
     source          1. .1400
                     /organism="Malus x domestica"
                     /cultivar="Granny Smith"
                     /db_xref="taxon:3750"
                     /tissue_type="fruit"
                     /dev_stage="ripening"
                     /note="authority: Malus domestica L. Borkh"
     CDS             <1. .1385
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                     /codon_start=3
                     /product="ACC synthase"
                     /protein_id="AAG28795.1"
                     /db_xref="GI:11066996"
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                     WLAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLV
                     LTAGATSANETFIFCLADPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQI
                     TETALEEAYQEAEKRNLRVKGVLVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDE
                     IYSGTAFSSPSFISVMEVLKDRNCDENSEVWQRVHVVYSLSKDLGLPGFRVGAIYSND
                     DMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKKLVSGLQK
                     SGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPGSSCHCTEPGW
                     FRVCFANLPERTLDLAMQRLKAFVGEYYNVPEVNGGSQSSHLSHSRRQSLTKWVSRLS
                     FDDRGPIPGR"
BASE COUNT      379 a    365 c    310 g    346 t
ORIGIN

  Query Match             27.4%;  Score 110.8;  DB 8;  Length 1400;
  Best Local Similarity   57.9%;  Pred. No. 3.9e-24;
  Matches  234;  Conservative    0;  Mismatches  167;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | |||||  ||  |  | ||||  |||||||||  || ||||  |  ||  |  |  |
Db     789 GGCCTTCCGGGTTTTCGAGTTGGCGCCATCTACTCCAACGACGACATGGTTGTGGCCGCC 848

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || | |||  || | ||  |||         ||||  |||  || |||| | | |||  ||
Db     849 GCTACAAAAATGTCAAGCTTTGGTCTTGTTTCTTCTCAAACTCAGCACCTTCTCTCCGCC 908

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           |||||  ||  ||||      |||||  | ||  | |||  |  |  |||       | |||||||
Db     909 ATGCTATCCGACAAAAAACTCACTAAGAACTACATAGCCGAGAACCACAAAAGACTCAAA 968

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             |    |         ||||  | ||  ||  |||||   |||||  | |||    |  |
Db     969 CAACGTCAGAAAAAGCTCGTCTCCGGCCTT-CAGAAATCTGGCATTAGCTGCCTCAACGG 1027

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  |  ||||  | |  |||||||  || |||||    ||| || | ||| ||| |
Db    1028 CAATGCTGGCT--TGTTCTGTTGGGTGGATATGAGGCACTTGCTTAGGTCCAACACCTTT 1085

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            |||  ||  | |||||  ||| | ||| |  || ||   | | |  | ||  |  ||||
Db    1086 GAAGCCGAAATGGAGCTCTGGAAAAAGATTGTATACGAAGTTCACCTCAATATATCTCCT 1145

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || | |||||||||  |  ||||| || |  ||  |  ||||
Db    1146 GGATCGTCTTGTCATTGCACGGAACCTGGTTGGTTCCGTGTCTG 1189


RESULT 13
MSU03294
LOCUS       MSU03294                1618 bp    mRNA    linear   PLN 18-NOV-1993
DEFINITION  Malus sylvestris 1-aminocyclopropane-1-carboxylate synthase mRNA,
            partial cds.
ACCESSION   U03294
VERSION     U03294.1  GI:417971
KEYWORDS    .
SOURCE      Malus sylvestris.
  ORGANISM  Malus sylvestris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE   1  (bases 1 to 1618)
  AUTHORS   Dong,J.G., Kim,W.T., Yip,W.K., Thompson,G.A., Li,L., Bennett,A.B.
            and Yang,S.F.
  TITLE     Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate
            synthase and expression of its mRNA in ripening apple fruit
  JOURNAL   Planta 185, 38-45 (1991)
REFERENCE   2  (bases 1 to 1618)
  AUTHORS   Dong,J.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-1993) Jian G. Dong, Vegetable Crops, University
            of California at Davis, Mann Lab, Davis, CA 95616-8631, USA
FEATURES             Location/Qualifiers
     source          1. .1618
                     /organism="Malus sylvestris"
                     /cultivar="Golden Delicious"
                     /db_xref="taxon:3752"
                     /clone="pAAS2"
                     /tissue_type="fruit"
                     /clone_lib="Library pCGN1703"
                     /dev_stage="ripening"
                     /note="Mill"
     old_sequence    1. .1618
                     /citation=[1]
     CDS             <1. .1395
                     /codon_start=1
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                     synthase"
                     /protein_id="AAA03472.1"
                     /db_xref="GI:417972"
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                     LLESWLAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAKIRGNKVTFDP
                     NHLVLTAGATSANETFIFCLADPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSN
                     GFQITETALEEAYQEAEKRNLRVKGVLVTNPSNPLGTTMTRNELYLLLSFVEDKGIHL
                     ISDEIYSGTAFSSPSFISVMEVLKDRNCDENSEVWQRVHVVYSLSKDLGLPGFRVGAI
                     YSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKKLVS
                     GLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPGSSCHCT
                     EPGWFRVCFANLPERTLDLAMQRLKAFVGEYYNVPEVNGGSQSSHLSHSRRQSLTKWV
                     SRLSFDDRGPIPGR"
BASE COUNT      437 a    398 c    351 g    432 t
ORIGIN

  Query Match             27.4%;  Score 110.8;  DB 8;  Length 1618;
  Best Local Similarity   57.9%;  Pred. No. 4e-24;
  Matches  234;  Conservative    0;  Mismatches  167;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | |||||  ||  |  | ||||  |||||||||  || ||||  |  ||  |  |  |
Db     799 GGCCTTCCGGGTTTTCGAGTTGGCGCCATCTACTCCAACGACGACATGGTTGTGGCCGCC 858

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || | |||  || | ||  |||         ||||  |||  || |||| | | |||  ||
Db     859 GCTACAAAAATGTCAAGCTTTGGTCTTGTTTCTTCTCAAACTCAGCACCTTCTCTCCGCC 918

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           |||||  ||  ||||      |||||  | ||  | |||  |  |  |||       | |||||||
Db     919 ATGCTATCCGACAAAAAACTCACTAAGAACTACATAGCCGAGAACCACAAAAGACTCAAA 978

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             |    |         ||||  | ||  ||  |||||   |||||  | |||    |  |
Db     979 CAACGTCAGAAAAAGCTCGTCTCCGGCCTT-CAGAAATCTGGCATTAGCTGCCTCAACGG 1037

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  |  ||||  | |  |||||||  || |||||    ||| || | ||| ||| |
Db    1038 CAATGCTGGCT--TGTTCTGTTGGGTGGATATGAGGCACTTGCTTAGGTCCAACACCTTT 1095

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            |||  ||  | |||||  ||| | ||| |  || ||   | | |  | ||  |  ||||
Db    1096 GAAGCCGAAATGGAGCTCTGGAAAAAGATTGTATACGAAGTTCACCTCAATATATCTCCT 1155

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || | |||||||||  |  ||||| || |  ||  |  ||||
Db    1156 GGATCGTCTTGTCATTGCACGGAACCTGGTTGGTTCCGTGTCTG 1199


RESULT 14
MDO011518
LOCUS       MDO011518               1633 bp    DNA     linear   PLN 23-OCT-1998
DEFINITION  Malus domestica acc synthase gene, exons 1-4, partial.
ACCESSION   AJ011518
VERSION     AJ011518.1  GI:3790174
KEYWORDS    1-aminocyclopropane-1-carboxilic synthase; acc synthase gene.
SOURCE      Malus x domestica.
  ORGANISM  Malus x domestica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE   1  (bases 1 to 1633)
  AUTHORS   Castiglione,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1998) Castiglione S., Biologia, Universita degli
            Studi di Milano, Via Celoria, 26 - 20133 Milano-IT, 20133, ITALIA
REFERENCE   2  (bases 1 to 1633)
  AUTHORS   Castiglione,S. and Bazzocchi,C.
  TITLE     Molecular analysis of ACC synthase and oxidase in Golden Delicious
            apple cultivar
  JOURNAL   Unpublished
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3750"
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                     /gene="acc synthase"
                     /codon_start=2
                     /product="1-aminocyclopropane -1-carboxilic synthase"
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                     /db_xref="GI:3790175"
                     /translation="NTNGIIQMGLAENQLCFDLLESWLAKNPEAAAFKKNGESIFAEL
                     ALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGATSANETFIFCLADPGEA
                     VLIPTPYYPRFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQEAEKRNLRVKGV
                     LVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDR
                     NCDENSEVWQRVHVVYSLSKDLGLPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQH
                     LLSAMLSDKKLTKNYIAENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDMRHLL
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                     FVGEYYNVPEV"
     exon            1. .43
                     /gene="acc synthase"
                     /number=1
     intron          44. .163
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                     /number=1
     exon            164. .299
                     /gene="acc synthase"
                     /number=2
     intron          300. .430
                     /gene="acc synthase"
                     /number=2
     exon            431. .586
                     /gene="acc synthase"
                     /number=3
     intron          587. .759
                     /gene="acc synthase"
                     /number=3
     exon            760. .1633
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                     /number=4
BASE COUNT      455 a    385 c    313 g    480 t
ORIGIN

  Query Match             27.4%;  Score 110.8;  DB 8;  Length 1633;
  Best Local Similarity   57.9%;  Pred. No. 4e-24;
  Matches  234;  Conservative    0;  Mismatches  167;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | ||||| ||  |  | ||||  |||||||| || |||| |  ||  |  | |
Db    1146 GGCCTTCCGGGTTTTCGAGTTGGCGCCATCTACTCCAACGACGACATGGTTGTGGCCGCC 1205

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || | |||  || | || |||      ||||  |||  || |||| | | |||  ||
Db    1206 GCTACAAAAATGTCAAGCTTTGGTCTTGTTTCTTCTCAAACTCAGCACCTTCTCTCCGCC 1265

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||||| || ||||      |||||  | || | ||| |  |  |||       | |||||||

Db    1266 ATGCTATCCGACAAAAAACTCACTAAGAACTACATAGCCGAGAACCACAAAAGACTCAAA 1325

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             |    |        ||||  | ||  ||  |||||   |||||  | |||    |  |
Db    1326 CAACGTCAGAAAAAGCTCGTCTCCGGCCTT-CAGAAATCTGGCATTAGCTGCCTCAACGG 1384

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  |  ||||  | |  |||||||  || |||||    ||| || | ||| ||| |
Db    1385 CAATGCTGGCT--TGTTCTGTTGGGTGGATATGAGGCACTTGCTTAGGTCCAACACCTTT 1442

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |||  ||  | |||||  ||| | ||| |  || ||   | | |  | ||  |  ||||
Db    1443 GAAGCCGAAATGGAGCTCTGGAAAAAGATTGTATACGAAGTTCACCTCAATATATCTCCT 1502

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || | |||||||||| |  ||||| || |  ||  |  ||||
Db    1503 GGATCGTCTTGTCATTGCACGGAACCTGGTTGGTTCCGTGTCTG 1546


RESULT 15
AB015624
LOCUS       AB015624               1778 bp    mRNA    linear   PLN 01-APR-1999
DEFINITION  Pyrus pyrifolia mRNA for 1-aminocyclopropane-1-carboxylic acid
            synthase, complete cds.
ACCESSION   AB015624
VERSION     AB015624.1  GI:4586425
KEYWORDS    1-aminocyclopropane-1-carboxylic acid synthase.
SOURCE      Pyrus pyrifolia (strain:Ninomiya) ripening fruit cDNA to mRNA.
  ORGANISM  Pyrus pyrifolia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
REFERENCE   1  (sites)
  AUTHORS   Itai,A., Kawata,T., Tanabe,K., Tamura,F., Uchiyama,M., Tomomitsu,M.
            and Shiraiwa,N.
  TITLE     Identification of 1-aminocyclopropane-1-carboxylic acid synthase
            genes controlling the ethylene level of ripening fruit in Japanese
            pear (Pyrus pyrifolia Nakai)
  JOURNAL   Mol. Gen. Genet. 261 (1), 42-49 (1999)
  MEDLINE   99168766
REFERENCE   2  (bases 1 to 1778)
  AUTHORS   Itai,A., Tomomitsu,M., Tanabe,K. and Tamura,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-1998) Akihiro Itai, Faculty of Agriculture,
            Tottori University, Laboratory of Horticultural Science; Koyama-cho
            Minami 4-101, Tottori, Tottori 680-8553, Japan
            (E-mail:itai@pear.agr.tottori-u.ac.jp, Tel:81-857-31-6749,
            Fax:81-857-31-6749)
FEATURES             Location/Qualifiers
     source          1. .1778
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                     /strain="Ninomiya"
                     /db_xref="taxon:3767"
                     /tissue_type="fruit"
                     /dev_stage="ripening"
     gene            1. .1778
                     /gene="pPPACS1"
     CDS             87. .1508
                     /gene="pPPACS1"
                     /codon_start=1
                     /product="1-aminocyclopropane-1-carboxylic acid synthase"
                     /protein_id="BAA76389.1"
                     /db_xref="GI:4586426"
                     /translation="MRMLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIQMG
                     LAENQLCFDLLESWLAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEI
                     RGNKVTFDPNHLVLTAGATSANETFIFCLADPGEAFLIPTPYYPGFDRDLKWRTGVEI
                     VPIHCTNSNGFQITETALEEAYQEAEKCNLRVKGVLVTNPSNPLGTTMTRNELYLLLS
                     FVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRNCDENFEVWQRVHVVYSLSKDLG
                     LPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRL
                     KQRQKNLVSGLQKAGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNI
                     SPGSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVGEYYNVPEVNGRSQSSHLSHS
                     RGQSLTKWVSRLSFDDRCPIHGR"
BASE COUNT      481 a    439 c    369 g    489 t
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ORIGIN

Query Match 27.4%; Score 110.8; DB 8; Length 1778;
Best Local Similarity 57.9%; Pred. No. 4e-24;
Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;

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Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     912 GGCCTTCCGGGTTTTCGGGTTGGCGCCATTTACTCCAACGACGACATGGTTGTGGCCGCC 971

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     972 GCTACAAAAATGTCAAGCTTTGGTCTTGTTTCTTCTCAAACTCAGCACCTTCTCTCCGCC 1031

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db    1032 ATGCTATCCGACAAGAAACTCACTAAGAACTACATAGCCGAGAACCACAAAAGACTCAAA 1091

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db    1092 CAACGTCAGAAAAATCTCGTCTCCGGCCTT-CAGAAAGCTGGCATTAGCTGCCTCAATGG 1150

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db    1151 CAATGCTGGCT--TGTTCTGTTGGGTGGATATGAGGCACTTGCTTAGGTCAAACACCTTT 1208

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db    1209 GAAGCCGAAATGGAGCTCTGGAAAAAGATTGTATACGAAGTTCACCTCAATATCTCTCCT 1268

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1269 GGATCGTCTTGTCATTGCACGGAACCTGGTTGGTTCCGTGTCTG 1312
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Search completed: March 11, 2003, 01:20:16
Job time : 1686 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:41:37 ; Search time 1211 Seconds
(without alignments)
5402.953 Million cell updates/sec

Title: US-09-975-842-1
Perfect score: 404
Sequence: 1 gggttgccggggttcaggat.....cccggctactttagcctctg 404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	194.8	48.2	664	13	BM437295	BM437295 VVA017C10
	2	174	43.1	503	12	BF425479	BF425479 su56c02.y
c	3	168	41.6	746	14	BQ118313	BQ118313 EST603889
	4	164.8	40.8	480	10	AW760199	AW760199 sl59c09.y
	5	148.4	36.7	654	14	BQ764374	BQ764374 EBan01_SQ
c	6	147.8	36.6	685	10	AV782646	AV782646 AV782646
c	7	145.6	36.0	550	14	BM953903	BM953903 sam67f01.
	8	143.6	35.5	629	13	BJ447315	BJ447315 BJ447315
	9	140	34.7	410	10	BE209956	BE209956 so37b07.y
	10	136.8	33.9	697	14	BQ863242	BQ863242 QGC23F17.
	11	127.6	31.6	616	9	AU238159	AU238159 AU238159
	12	119.8	29.7	515	10	AW064832	AW064832 ST36D01 P
	13	118	29.2	483	10	AW040322	AW040322 EST283186
c	14	112.6	27.9	423	10	AV808550	AV808550 AV808550
c	15	107.2	26.5	420	10	AV820681	AV820681 AV820681
c	16	96.8	24.0	803	17	BH708432	BH708432 BOHTU20TF
	17	96.4	23.9	1588	11	AY104732	AY104732 zea mays
	18	92.8	23.0	520	12	BF648947	BF648947 NF054C12E
	19	89.6	22.2	352	14	BQ793884	BQ793884 EST 2822
	20	87.6	21.7	700	14	BQ246577	BQ246577 TaE15008D
	21	85.2	21.1	651	12	BF649567	BF649567 NF079G12E
	22	84.8	21.0	660	14	BQ148323	BQ148323 NF067A11F
	23	83.8	20.7	656	9	AL505273	AL505273 AL505273
	24	82.2	20.3	496	9	AI993687	AI993687 701497137
	25	82	20.3	819	13	BI421967	BI421967 EST532633
c	26	80.8	20.0	725	14	BQ509056	BQ509056 EST616471
	27	80.4	19.9	704	13	BI921823	BI921823 EST541726
	28	78.8	19.5	691	14	BQ087604	BQ087604 Cri_9_F11
c	29	78.4	19.4	176	14	BQ118332	BQ118332 EST603908
	30	78.2	19.4	537	9	AI894662	AI894662 EST264105
	31	76	18.8	538	10	BE436538	BE436538 EST407616
c	32	75.8	18.8	344	17	CNS00PXP	AL085099 Arabidops
	33	75.2	18.6	140	10	AV834755	AV834755 AV834755
	34	73.6	18.2	851	17	BH517544	BH517544 BOGBR16TR
c	35	73.4	18.2	623	10	AW560294	AW560294 EST315342
c	36	72	17.8	511	12	BE821561	BE821561 GM700014B
	37	71.2	17.6	569	9	AI899193	AI899193 EST268636
	38	70.6	17.5	505	9	AA650853	AA650853 30967 Lam
	39	70.4	17.4	528	13	BM372377	BM372377 EBro03_SQ
	40	68.8	17.0	522	13	BI315805	BI315805 saf63e08.
	41	68.6	17.0	607	17	B61942	B61942 T19L13TR TA
	42	67.6	16.7	503	9	AI794804	AI794804 sb70f01.y
	43	64.4	15.9	658	9	AI487009	AI487009 EST245331
	44	64.2	15.9	632	9	AI485399	AI485399 EST243720
	45	64.2	15.9	636	9	AI485332	AI485332 EST243653

ALIGNMENTS

RESULT 1
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LOCUS BM437295 664 bp mRNA linear EST 31-JAN-2002
DEFINITION VVA017C10_54085 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera cDNA clone VVA017C10 5, mRNA sequence.
ACCESSION BM437295
VERSION BM437295.1 GI:18459017
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 664)
AUTHORS Cramer,G.R. and Cushman,J.C.
TITLE An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer

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            Plate: 017  row: C  column: 10
            Seq primer: T3 20mer
            High quality sequence stop: 664.
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                      /clone_lib="An expressed sequence tag database for abiotic
                      stressed leaves of Vitis vinifera var. Chardonnay"
                      /tissue_type="leaf"
                      /dev_stage="juvenile and adult"
                      /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Library construction was performed
                      according to Stratagene's  recommended protocol for the
                      Lambda UniZapXR vector and cDNA synthesis kit."
BASE COUNT      195 a    119 c    152 g    197 t      1 others
ORIGIN

  Query Match             48.2%;  Score 194.8;  DB 13;  Length 664;
  Best Local Similarity   71.2%;  Pred. No. 2e-55;
  Matches  285;  Conservative    0;  Mismatches  112;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
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Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
Db      96 AGAAACTCTCAAGGTTTTCTTCCATTTCAGCTCCAACCCAGTGTTTGGTTATCTCCATGC 155

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
Db     156 TTTCAGATATAAGATTCATACAAAAGTTCATTCAGACCAACAGAGAGAGGCTTCAAAGAA 215

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
Db     216 TGTATACTAAATTCGTGGC-AGGGTTGAAACAATTAGGAATTGAGTGCATGCGGAGCAGT 274

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
Db     275 GGGGGCT--TCTACTGTTGGGCTGACATGAGGGGATTAATCCGCTCTTACAGTGAGAAAG 332

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
Db     333 GGGAGCTCGAGCTATGGAACAAATTGTTGAATATAGCAAAGATAAATGTAACTCCAGGAT 392

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db     393 CTTCTTGTCACTGTATTGAACCTGGATGGTTCCGCTGTTG 432


RESULT 2
BF425479
LOCUS       BF425479                503 bp    mRNA    linear   EST 06-DEC-2001
DEFINITION  su56c02.y1 Gm-c1069 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1069-891 5' similar to TR:Q9SNN8 Q9SNN8 SIMILAR TO
            1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE. ;, mRNA sequence.
ACCESSION   BF425479
VERSION     BF425479.1  GI:11413468
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 503)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Insert Length: 1667   Std Error: 0.00
            High quality sequence stop: 422.
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                      etiolated seedling"
                      /lab_host="DH10B"
                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                      XhoI; The cDNA library was constructed from mRNA isolated
                      from degenerating cotyledons of 9-10 day old etiolated
                      seedlings for the cultivar Williams. Complementary DNA was
                      synthesized from mRNA using a primer consisting of a
                      poly(dT) sequence with a XhoI restriction site. EcoRI
                      adapters were ligated  to the blunt-ended cDNA fragments
                      followed by XhoI digestion. The cDNA  fragments were
                      directionally cloned into the EcoRI-XhoI restriction site
                      of  the pBluescript vector. The ligated cDNA fragments
                      were transformed into  DH10B host cells (GibcoBRL). This
                      library was constructed in the laboratory  of Dr. Randy
                      Shoemaker."
BASE COUNT      116 a     86 c    134 g    167 t
ORIGIN

  Query Match             43.1%;  Score 174;  DB 12;  Length 503;
  Best Local Similarity   68.0%;  Pred. No. 2.5e-48;
  Matches  272;  Conservative    0;  Mismatches  125;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
Db      37 TTCCAGGTTTGAAGGTGGGTGTTATCTACTCTTATAATGACAATGTCGTGGCTGCTTCTA 96

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
Db      97 GCAAATTGGCAAGGTTCTCCACTGTTTCTGCCCCAACCCAAAGATTGCTCATCTCCATGC 156

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
Db     157 TTTCAGATACAAGTTTTGTGCAAAAATTTATTGAGGTTAACAGGTTGAGGCTGCGGAAAA 216

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
Db     217 TGTATAATACATTTGTTGC-GGGGCTGAAGCAGTTGGGGATTGAGTGCACTAGGAGCAGT 275

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
Db     276 GGTGG--TTTTTGCTGCTGGGCTGACATGAGCAGGTTGATTGGCTCTTACAGTGAAAAGG 333

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
Db     334 GAGAGCTTGAGCTCTGGGATAGATTGTTGAATGTTGCTAAGATCAATGTTACCCCGGGTT 393

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db     394 CCTCTTGTCACTGTATTGAACCTGGATGGTTTCGTTTTTG 433
```

```
RESULT 3
BQ118313/c
LOCUS       BQ118313                746 bp    mRNA    linear   EST 17-APR-2002
DEFINITION  EST603889 mixed potato tissues Solanum tuberosum cDNA clone STMEA01
            3' end, mRNA sequence.
ACCESSION   BQ118313
VERSION     BQ118313.1  GI:20170275
KEYWORDS    EST.
SOURCE      potato.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
            Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
            Karamycheva,S.A.
  TITLE     Generation of a set of potato cDNA clones for microarray analyses
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato@tigr.org
            This clone is available through the Research Genetics, contact the
            Research Genetics for further information 1-800-711-6195 or
            cdna@resgen.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Solanum tuberosum"
                     /cultivar="Kennebec or Binjte"
                     /db_xref="taxon:4113"
                     /clone="STMEA01"
                     /clone_lib="mixed potato tissues"
                     /tissue_type="mixed tissues"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Combination of untreated and Phytophthora
                     infestans-treated libraries of stolons, leaves, leaflets,
                     axillary buds of stem explants, petioles, germinating eyes
                     , tubers, or roots."
BASE COUNT      238 a    185 c    109 g    214 t
ORIGIN

  Query Match           41.6%;  Score 168;  DB 14;  Length 746;
  Best Local Similarity   67.5%;  Pred. No. 3.4e-46;
  Matches  266;  Conservative    0;  Mismatches  125;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
           |||| ||||| ||| | || ||| | || |||| ||| ||||| ||  |  |  |  | |
Db     594 TGCCAGGGTTTAGGCTCGGTGTTCTGTATTCCTTCAATGAGAATGTTGTGGCAGCATCTA 535

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           |||||||||| |||||||   ||  |||||| || || ||| || |  | || |  ||||
Db     534 AAAAGTTGACAAGATTTTGTGCCGCTTCAGCACCAACACAGAGCCTATTAGTTGCAATGC 475

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | || ||  |  ||||||   |  | |  ||      ||||||| || | |    | |
Db     474 TTTCAGATGCTGGGTTCATCAAGGATTATATGAGAACAAACAGAGAGAGATTGCGCAAAG 415

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
           |||  |    ||| |||||  ||  | ||  || | |||||   ||||| | | |||||
Db     414 TGTTTGACTTATTTGTGGC-AGGTCTAAAACAATTGGGCATTGAATGCATGAACAGCAGT 356

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
           | ||||  || ||||||||||   | ||||||||||||||| |  | || |  ||||| |
Db     355 GCAGGC--CTGTATTGTTGGGTTAATATGAGCGGATTGATTTGCCCTTATAATGAAAAGG 298

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
           ||||||| ||||| ||||| ||| |  | ||  | |||||| |||||| ||||| || |
Db     297 GAGAGCTTGAGCTGTGGGAGAAGCTCTTGAATGTAGCTAAGATAAACGTGACTCCAGGGT 238

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAG 398
           |   ||| |||||||||||||| || |  || ||
Db     237 CAGCTTGCCATTGTATTGAACCTGGATGGTTCAG 204


RESULT 4
AW760199
LOCUS       AW760199                480 bp    mRNA    linear   EST 03-DEC-2001
DEFINITION  s159c09.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1027-5609 5' similar to TR:Q43201 Q43201
            1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION   AW760199
VERSION     AW760199.1  GI:7692084
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            High quality sequence stop: 418.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-5609"
                     /clone_lib="Gm-c1027"
                     /tissue_type="cotyledons of 3- and 7-day-old Williams
                     seedlings"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; This cDNA library was constructed from mRNA isolated
                     from cotyledons of 3- and 7-day-old Williams seedlings
                     which were propagated on paper towels with distilled
                     water.  The cotyledons were flash-frozen in liquid
                     nitrogen, then lyophilized for 72 hours.  Unequal amounts
                     of mRNA was used for cDNA synthesis.  Stratagene's cDNA
                     Synthexix Kit (catalog number 200401) was used to
                     synthesize the cDNA.  First- stranded synthesis was
                     performed with 5-methyl dCTP, hence the ligated cDNA was
                     hemimethylated.  A modification of Stratagene's
                     first-strand  synthesis primer was used.  An anchor
                     nucleotide (V=A, C, or G) was added to the 3' end of the
                     primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18] to anchor
                     the primer at the 5' end of the poly(A) tract.  After
                     second- strand synthesis, the cDNA ends were filled in
                     with cloned Pfu DNA, ligated to EcoRI adapters and
                     subsequently phosphorylated.  The XhoI site within the
                     first-strand synthesis primer was then restricted by
                     digestion with XhoI; all XhoI sites in the cDNA would be
                     protected by their hemimethylated status.  The cDNA
                     constructs were size-fractionated with a 500 bp cutoff,
                     using GibcoBRL Life Technologies' cDNA Size Fractionation
                     column.  The column eluent was then ligated into
                     Stratagene's pBluescript(tm) II XR Predigested vector
```

(pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
BASE COUNT 118 a 86 c 132 g 144 t
ORIGIN

Query Match 40.8%; Score 164.8; DB 10; Length 480;
Best Local Similarity 67.6%; Pred. No. 3.5e-45;
Matches 261; Conservative 0; Mismatches 122; Indels 3; Gaps 2;

```
Qy      3 GTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 62
          | | || || || | | |||| |||||||||| || || || || ||  |  || || |
Db     93 GGTTCCAGGTTTAAAGGTGGGTGTTATCTACTCTTATAATGACAATGTCGTGGCTGCTTC 152

Qy     63 CAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTAT 122
            |  |  ||| | || || ||  |  |||| || || || ||  | |||||| ||   ||
Db    153 TAGCATATTGGCAAGGTTCTCCACTGTTTCTGCCCCAACCCAAAGATTGCTCATCTCCAT 212

Qy    123 GCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAG 182
          |||||| || ||  | ||    ||||| || || ||||| ||||||  ||  ||    |
Db    213 GCTCTCAGATACAAGTTTTGTGCAAAATTTTATTGAGGTTAACAGATTGAGGCTGCGGAA 272

Qy    183 AATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCA 242
          ||||||   | |||| || ||   || ||||| |  | || ||    |||||    ||||
Db    273 AATGTATAATACATTTGTTGC-ACGGCTGAAGCAGTTGGGGATTGAGTGCACTAGGAGCA 331

Qy    243 GCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAA 302
          | || ||  ||| |  || ||||| ||||||||| | |||||||| || ||||| ||||
Db    332 GTGGTGG--TCTTTGCTGCTGGGCTGACATGAGCAGGTTGATTCGCTCTTACAGTGAAAA 389

Qy    303 AGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGG 362
          || ||||| |||| ||||| |  ||| | ||  |||||||| | || ||||| || ||
Db    390 GGGGGAGCTTGAGCTCTGGGATAGATTGTTGAATGTTGCTAAGATCAATGTTACCCCGGG 449

Qy    363 TTCTTGTTGTCATTGTATTGAACCCG 388
            || |  ||||| || |||||||| |
Db    450 ATCATCATGTCACTGCATTGAACCTG 475
```

RESULT 5
BQ764374
LOCUS BQ764374 654 bp mRNA linear EST 26-JUL-2002
DEFINITION EBan01_SQ005_M15_R anther, yellow stage, no treatment, cv Optic, EBan01 Hordeum vulgare cDNA clone EBan01_SQ005_M15 5', mRNA sequence.
ACCESSION BQ764374
VERSION BQ764374.1 GI:21972846
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 654)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
FEATURES Location/Qualifiers
source 1. .654
/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBan01_SQ005_M15"
/clone_lib="anther, yellow stage, no treatment, cv Optic, EBan01"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from anthers dissected from developing flowers in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
BASE COUNT 168 a 143 c 184 g 158 t 1 others
ORIGIN

Query Match 36.7%; Score 148.4; DB 14; Length 654;
Best Local Similarity 64.0%; Pred. No. 1.7e-39;
Matches 256; Conservative 0; Mismatches 141; Indels 3; Gaps 2;

```
Qy      5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
            || | |||||  || | || || || || || ||||| || | | |  |      | |||
Db     18 TGGCAGGGTTTCGGGTTGGAGTCATATATTCGTACAATGAAAGCATCGTGGAGGCAGCCG 77

Qy     65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
            ||| |  | ||||| |||||| | ||| | ||||| |||||| |||| || |  ||||
Db     78 CTAAGATTGCTAGATTCTCATCCGTGTCAACCCCGACCCAGCGCCTGCTTGTTGCCATGC 137

Qy    125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
          | || |||  |  ||| |      || | | |  | || ||||||| ||  ||  | |
Db    138 TTTCAGACCAGAAGTTTATCTCGAATTACCTGAAAGTTAACAGAGAGAGGCTGCACAAGG 197

Qy    185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
            ||||  |    |||| |   |  |||||  |  | ||| ||   |||    | ||||||
Db    198 CGTACAATTTGCTCGTTG-ATGCTTTGAAACAGGTGGGCGTCGAGTGCTTCAAGAGCAGC 256

Qy    245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
          |||||  |  |||| || ||||| || ||||||   || || || || |||||||| ||||
Db    257 GGAGGAT--TCTACTGCTGGGCGGATATGAGCAAGTTCATCCGGTCTTACAGCGAGAAAG 314

Qy    305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
          | || | |  ||| |||||||  | || |  |    || ||||| || || || ||||
Db    315 GGGAACGCAGGCTTTGGGACAGGCTGTTGGAGGAGGCGAAGGTCAATGTCACCCCAGGTT 374

Qy    365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          | | ||| ||||| ||||| || || |  |||||   |||
Db    375 CATCTTGCCATTGCATTGAGCCTGGATGGTTTAGGTGCTG 414
```

RESULT 6
AV782646/c
LOCUS AV782646 685 bp mRNA linear EST 28-MAR-2002
DEFINITION AV782646 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-20-B08 3', mRNA sequence.
ACCESSION AV782646
VERSION AV782646.1 GI:19801436
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 685)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359

```
            Fax: 81-298-36-9060
            Email: mseki@rtc.riken.go.jp
            An Arabidopsis full-length cDNA library was constructed essentially
            as reported previously (Seki et al., 1998). This clone is in a
            modified pBluescript vector as a SstI/XhoI insert. Please visit our
            web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .685
                      /organism="Arabidopsis thaliana"
                      /db_xref="taxon:3702"
                      /clone="RAFL04-20-B08"
                      /clone_lib="RAFL4"
                      /dev_stage="rosette plants"
                      /lab_host="SOLR"
                      /note="Site_1: SstI; Site_2: XhoI; subjected to
                      cold-treated(1,2,5,10,24 hr)"
BASE COUNT      193 a    163 c    125 g    204 t
ORIGIN

  Query Match             36.6%;  Score 147.8;  DB 10;  Length 685;
  Best Local Similarity   63.8%;  Pred. No. 2.8e-39;
  Matches  256;  Conservative    0;  Mismatches  142;  Indels    3;  Gaps    2;

Qy       4 TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
           || | |||| | ||    |  | |||||||||| | ||||||||  ||  |  |  || |
Db     529 TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 470

Qy      64 AAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATG 123
           | |||| | ||||   | ||| |  | ||| |||| || || |  |||||  |
Db     469 AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 410

Qy     124 CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
            ||||  |  |          ||| |  ||  |  |    |||||   || | |  | ||
Db     409 ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 350

Qy     184 ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
           || ||| | |   ||||||  |||||||||  |  | || |||   |||||   |||||
Db     349 ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 291

Qy     244 CGGAGGCTTCTCTATTGTTGGGCCGACATGAGCCGGATTGATTCGATCCTACAGCGAAAAA 303
            |||||  |  |||| ||||||||  || ||| | |||||||||  ||| ||||||||||||
Db     290 TGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTGATTTCATCTTACAGCGAAAAA 233

Qy     304 GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGT 363
           || ||| | ||||| ||| ||||| |  | |||||||  ||| | || || |  || ||  ||
Db     232 GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 173

Qy     364 TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           |||||||||||  |||||  |||||  ||  |  ||  |  ||||
Db     172 TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG 132


RESULT 7
BM953903/c
LOCUS       BM953903                 550 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  sam67f01.y1 Gm-c1069 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1069-4489 5' similar to TR:Q9SNN8 Q9SNN8 SIMILAR TO
            1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE. ;, mRNA sequence.
ACCESSION   BM953903
VERSION     BM953903.1  GI:19452493
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@resgen.com web site:
            www.resgen.com
            Possible reversed clone: similarity on wrong strand
            High quality sequence stop: 421.
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Glycine max"
                      /db_xref="taxon:3847"
                      /clone="SOYBEAN CLONE ID: Gm-c1069-4489"
                      /clone_lib="Gm-c1069"
                      /tissue_type="Degenerating cotyledons, 9-10 day old
                      etiolated seedling"
                      /lab_host="DH10B"
                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                      XhoI; The cDNA library was constructed from mRNA isolated
                      from degenerating cotyledons of 9-10 day old etiolated
                      seedlings for the cultivar Williams. Complementary DNA was
                      synthesized from mRNA using a primer consisting of a
                      poly(dT) sequence with a XhoI restriction site. EcoRI
                      adapters were ligated  to the blunt-ended cDNA fragments
                      followed by XhoI digestion. The cDNA  fragments were
                      directionally cloned into the EcoRI-XhoI restriction site
                      of  the pBluescript vector. The ligated cDNA fragments
                      were transformed into  DH10B host cells (GibcoBRL). This
                      library was constructed in the laboratory  of Dr. Randy
                      Shoemaker."
BASE COUNT      169 a    135 c     86 g    160 t
ORIGIN

  Query Match             36.0%;  Score 145.6;  DB 14;  Length 550;
  Best Local Similarity   63.4%;  Pred. No. 1.5e-38;
  Matches  255;  Conservative    0;  Mismatches  144;  Indels    3;  Gaps    2;

Qy       3 GTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGC 62
           | |  | || || ||  | || |||||  |  || | ||| ||||  ||  |  || ||||
Db     431 GCTTGCTGGCTTTAGAGTCGGGGTTATATGTTCATTCAATGAGAGTGTTTTGGCTGCTGC 372

Qy      63 CAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTAT 122
           ||| |||||||  ||||||||| || || || |||||||| ||| | ||  |        ||
Db     371 CAAGAAGTTGAGTAGATTTTCCTCTATATCCGCTCCGACCCAGAGGTTAGTTACTTCAAT 312

Qy     123 GCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAG 182
           ||| || || |   | || | ||   ||| | | ||    |||       | | |   |
Db     311 GCTTTCAGATAAAAGATTTATTCGGGAGTACTTTGAAACCAACCAGAAAAGAATACGACA 252

Qy     183 AATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCA 242
           | || ||| || ||| |||| |  | || |  ||||| || |||   ||  |  | ||||
Db     251 AGTGCACGATGAATTTGTGG-GTTGTTTAAGTAAACTAGGAATCAAGTGTGCCAAGAGCA 193

Qy     243 GCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAA 302
           | |  ||  | | || |||||||| || ||||| ||||| || ||| | || || || ||
Db     192 GTGCTGG--TATGTACTGTTGGGCTGATATGAGTGGATTAATCCGACCTTATAGTGAGAA 135

Qy     303 AGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGG 362
           ||||||  | ||  |||||||  ||||| | |   |||||||| | ||  | ||||| ||
Db     134 AGGAGAAATTGAATTATGGGAGAAGTTTTTGAGTGTTGCTAAGATCAATATAACTCCTGG 75

Qy     363 TTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||    || ||||| || ||||| || |  |||||  | ||
Db      74 GTCAGCCTGCCATTGCATAGAACCAGGATGGTTTAGGATTTG 33
```

```
RESULT 8
BJ447315
LOCUS       BJ447315                629 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  BJ447315 K. Sato unpublished cDNA library, cv. Akashinriki
            vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
            baak14o13 5', mRNA sequence.
ACCESSION   BJ447315
VERSION     BJ447315.1  GI:21125948
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 629)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .629
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Akashinriki"
                     /db_xref="taxon:112509"
                     /clone="baak14o13"
                     /clone_lib="K. Sato unpublished cDNA library, cv.
                     Akashinriki vegetative stage leaves"
                     /tissue_type="leaves"
                     /dev_stage="vegetative stage"
BASE COUNT      165 a    139 c    174 g    151 t
ORIGIN

  Query Match           35.5%;  Score 143.6;  DB 13;  Length 629;
  Best Local Similarity   63.8%;  Pred. No. 7.5e-38;
  Matches  250;  Conservative    0;  Mismatches  139;  Indels    3;  Gaps    2;

Qy      13 TTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCAAAAAGTTG 72
           ||| | | | | || || || || ||||| || | | |  |      | |||   ||| |
Db       3 TTCGGCACGAGGGTCATATATTCGTACAATGAAAGCATCGTGGAGGCAGCCGCTAAGATT 62

Qy      73 ACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCTCGGAC 132
             | ||||| |||||| | ||| | ||||| |||||| |||| || |  ||||| || |||
Db      63 GCTAGATTCTCATCCGTGTCAACCCCGACCCAGCGCCTGCTTGTTGCCATGCTTTCAGAC 122

Qy     133 ACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCT 192
             |  ||| |     || | | |  | || ||||||| ||  ||  | |    |||| |
Db     123 CAGAAGTTTATCTCGAATTACCTGAAAGTTAACAGAGAGAGGCTGCACAAGGCGTACAAT 182

Qy     193 GCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTT 252
               |||| |   |  |||||  |  | ||| ||   |||    | ||||||||||| |
Db     183 TTGCTCGTTG-ATGCTTTGAAACAGGTGGGCGTCGAGTGCTTCAAGAGCAGCGGAGGAT- 240

Qy     253 CTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGAGCTC 312
           |||| || ||||| || ||||||   || || || || |||||||| ||||| || | |
Db     241 -TCTACTGCTGGGCGGATATGAGCAAGTTCATCCGGTCTTACAGCGAGAAAGGGGAACGC 299

Qy     313 GAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTTGTTGT 372
             ||| |||||||  | || |  |    || ||||| || || || || ||||| | |||
Db     300 AGGCTTTGGGACAGGCTGTTGGAGGAGGCGAAGGTCAATGTCACCCCAGGTTCATCTTGC 359

Qy     373 CATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||||| ||||| || || |  |||||   |||
Db     360 CATTGCATTGAGCCTGGATGGTTTAGGTGCTG 391
```

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RESULT 9
BE209956
LOCUS       BE209956                410 bp    mRNA    linear   EST 04-DEC-2001
DEFINITION  so37b07.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1039-110 5' similar to TR:Q43201 Q43201
            1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION   BE209956
VERSION     BE209956.1  GI:8826235
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Insert Length: 1204   Std Error: 0.00
            High quality sequence stop: 409.
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1039-110"
                     /clone_lib="Gm-c1039"
                     /tissue_type="whole seedling without cotyledons"
                     /lab_host="DH10B"
                     /note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
                     XhoI; This cDNA library was constructed from mRNA isolated
                     from 2 week old seedlings with the cotyledons removed at
                     the time of harvest. The seedlings for the cultivar Ogden
                     were grown in a growth chamber using germination paper.
                     Complementary DNA was synthesized from mRNA using a primer
                     consisting of a poly(dT) sequence with a XhoI restriction
                     site. EcoRI adapters were ligated to the blunt-ended cDNA
                     fragments followed by XhoI digestion. The cDNA fragments
                     were directionally cloned into the EcoRI-XhoI restriction
                     site of the pBluescript vector. The ligated cDNA fragments
                     were transformed into DH10B host cells (Gibco BRL). This
                     library was constructed by Dr. Randy Shoemaker."
BASE COUNT       97 a     72 c    110 g    130 t      1 others
ORIGIN

  Query Match           34.7%;  Score 140;  DB 10;  Length 410;
  Best Local Similarity   68.4%;  Pred. No. 1.1e-36;
  Matches  223;  Conservative    0;  Mismatches  100;  Indels    3;  Gaps    2;

Qy      79 TTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCTCGGACACGCGG 138
           || ||  |  |||| || || || ||  | |||||| ||   ||||| || || ||  |
Db       1 TTCTCCACTGTTTCTGCCCCAACCCAAAGATTGCTCATCTCCATGCTTTCAGATACAAGT 60

Qy     139 TTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTC 198
           ||    ||||| || || ||||| |||||   ||  ||    | ||||||   | ||||
Db      61 TTTGTGCAAAAATTTATTGAGGTTAACAGGTTGAGGCTGCGGAAAATGTATAATACATTT 120

Qy     199 GTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTAT 258
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Db    121 GTTGC-GGGGCTGAAGCAGTTGGGGATTGAGTGCACTAGGAGCAGTGGTGG--TTTTTGC 177

Qy    259 TGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCTA 318

Db    178 TGCTGGGCTGACATGAGCAGGTTGATTGGCTCTTACAGTGAAAAGGGAGAGCTTGAGCTC 237

Qy    319 TGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTTGTTGTCATTGT 378

Db    238 TGGGATAGATTGTTGAATGTTGCTAAGATCAATGTTACCCCGGGTTCCTCTTGTCACTGT 297

Qy    379 ATTGAACCCGGCTACTTTAGCCTCTG 404

Db    298 ATTGAACCTGGATGGTTTCGTTTTTG 323


RESULT 10
BQ863242
LOCUS       BQ863242                697 bp    mRNA    linear   EST 14-AUG-2002
DEFINITION  QGC23F17.yg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
            QGC23F17, mRNA sequence.
ACCESSION   BQ863242
VERSION     BQ863242.1  GI:22248707
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGC23  row: F  column: 17.
FEATURES             Location/Qualifiers
     source          1. .697
                     /organism="Lactuca sativa"
                     /cultivar="Salinas"
                     /db_xref="taxon:4236"
                     /clone="QGC23F17"
                     /clone_lib="QG_ABCDI lettuce salinas"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_ABCDI lettuce salinas
                     TAG_TISSUE=flowers post-fertilized
                     TAG_SEQ=TGCCATCGGG"
BASE COUNT      201 a     70 c    181 g    245 t
ORIGIN

  Query Match             33.9%;  Score 136.8;  DB 14;  Length 697;
  Best Local Similarity   62.3%;  Pred. No. 1.7e-35;
  Matches  248;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    2;

Qy      7 CCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCAAA 66

Db    108 CCTGGTTTACGAGTCGGGGTTGTTTATTCGTTTGATAAAAACGTGTTGGAGGCATCGAAG 167

Qy     67 AAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTC 126

Db    168 AAATTGGTGAGATTTTCATCTGTGTCATCTTTGAACCAAAGAATGCTCGTTTCAATGCTT 227

Qy    127 TCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATG 186

Db    228 AATGATTCAAGATTTGTTGAAGGGTTTATAAAGATTAATAGAGAAAGAGTTGAGAAAATG 287

Qy    187 TACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGG 246

Db    288 AGTGATCTTTTTGTGG-GTGGTTTGAAGAGTTTGGGAATTGAGTGTATGAAAAGTGGTGG 346

Qy    247 AGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGA 306

Db    347 AGGGT--TTTATTGTTGGGCGGATTTGAGTGGTTTTATACGGCCTTATAGTGAAAAAGGT 404

Qy    307 GAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCT 366

Db    405 GAGCTTGAATTGTGGGAAAAGTTGTTGAATGTGGGAAAAGTCAATTCTACCCCTGGATCA 464

Qy    367 TGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404

Db    465 TCTTGTCATTGTGTAGAACCAGGGTGGTTTAGGTTTTG 502


RESULT 11
AU238159
LOCUS       AU238159                616 bp    mRNA    linear   EST 01-APR-2002
DEFINITION  AU238159 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-89-D04 5',
            mRNA sequence.
ACCESSION   AU238159
VERSION     AU238159.1  GI:19877328
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 616)
  AUTHORS   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
            Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
            Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu
            ,M., Hayashizaki,Y. and Shinozaki,K.
  TITLE     Large scale analysis of Arabidopsis full-length cDNA
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Motoaki Seki
            Plant Functional Genomics Research Group
            RIKEN Genomic Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-4359
            Fax: 81-298-36-9060
            Email: mseki@rtc.riken.go.jp
            An Arabidopsis full-length cDNA library was constructed essentially
            as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
            and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
            al., submitted for publication) digested with BamHI and SalI. This
            clone is in a modified pBluescript vector. Please visit our web
            site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
            details.
FEATURES             Location/Qualifiers
     source          1. .616
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
                     /clone="RAFL16-89-D04"
                     /clone_lib="RAFL16"
                     /lab_host="DH10B"
                     /note="Site_1: BamHI; Site_2: SalI; dark-grown"
BASE COUNT      172 a     99 c    154 g    188 t      3 others
```

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ORIGIN

  Query Match             31.6%;  Score 127.6;  DB 9;  Length 616;
  Best Local Similarity   60.8%;  Pred. No. 2.3e-32;
  Matches  243;  Conservative    0;  Mismatches  154;  Indels    3;  Gaps    2;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
           | || || || ||    || || ||||||||||   | ||  ||||  | | | |||| |
Db     147 TTCCTGGTTTTAGAGCTGGAGTCATCTACTCCTTTCATGAAGACGTAGTAAATGCTGCAA 206

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           | ||| ||| ||||||||||||   |  ||| ||     ||  |  | ||  ||  | | |
Db     207 AGAAGCTGATGAGATTTTCATCAGTGCCAGTTCTAGTTCAAAGGATACTTATCTCTCTAC 266

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | || ||     | |||| | |    | ||| |  | | ||||    |   ||      |
Db     267 TATCTGATGTAAGATTCATTGAGGGATACATGGCAGCACACAGGCAAAGGATCCGGGATA 326

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
           | |    |   || ||||   || |||||  || | || || | |||  | || ||  |
Db     327 AGCATATTCGGTTTGTGG-AAGGTTTGAAACAATTAGGAATACCATGTGCTGAGAGTGGT 385

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
           || || |  | ||||||||||  |||||||||| | ||  |   ||| ||||| || ||||
Db     386 GGTGGGT--TGTATTGTTGGGTAGACATGAGCAGTTTACTGACATCTTACAGTGAGAAAG 443

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
           |||| ||||||  |||  || ||| |  | |   |||||||| | || |  ||||| ||
Db     444 GAGAACTCGAGTTATTTGAGAAGCTATTGACTGTTGCTAAGATTAATGCCACTCCAGGAA 503

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           |    ||| ||||||| ||||| || |  || ||   |||
Db     504 CAGCCTGTTATTGTATAGAACCAGGTTGGTTCAGGTGCTG 543


RESULT 12
AW064832
LOCUS       AW064832                515 bp    mRNA    linear   EST 12-OCT-1999
DEFINITION  ST36D01 Pine TriplEx shoot tip library Pinus taeda cDNA clone
            ST36D01, mRNA sequence.
ACCESSION   AW064832
VERSION     AW064832.1  GI:6019904
KEYWORDS    EST.
SOURCE      loblolly pine.
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
  TITLE     The Pine Gene Discovery Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ross Whetten
            Forest Biotechnology Group
            North Carolina State University
            Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
            ,NC, 27695-8008
            Tel: 919-515-7800
            Fax: 919-515-7801
            Email: rosswhet@unity.ncsu.edu
            Seq primer: 5' lambda TriplEx2 Sequencing Primer.
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Pinus taeda"
                     /db_xref="taxon:3352"
                     /clone="ST36D01"
                     /clone_lib="Pine TriplEx shoot tip library"
                     /lab_host="E. coli BM25.8"
                     /note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
                     SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from
                     apex) were collected during the spring, frozen and used
                     for mRNA isolation. The SMART-PCR method (Clontech) was
                     used to prepare a library from 1 ug total RNA, using the
                     Lambda TriplEx vector. Plasmid subclones in pTriplEx were
                     recovered by cre-lox excision in E. coli strain BM25.8 and
                     sequenced from the 5' end."
BASE COUNT      140 a      88 c     119 g     154 t      14 others
ORIGIN

  Query Match             29.7%;  Score 119.8;  DB 10;  Length 515;
  Best Local Similarity   57.8%;  Pred. No. 1e-29;
  Matches  226;  Conservative    0;  Mismatches  163;  Indels    2;  Gaps    1;

Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
           | || || || ||  | || ||||| || || ||||| || || || ||||   ||||
Db      71 TTCCAGGTTTTAGAGTTGGAGTTATTTATTCTTACAATGATAAAGTCCTCAAAGCTGCTC 130

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           |  || || | ||||| |  ||  ||||  ||| ||| ||||  ||||||  |    ||||
Db     131 AGCAGATGTCAAGATTCTGCTCTGTTTCNTCTCAGACACAGCATTTGCTCATTAACATGC 190

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | |||||| | |  || |  ||  | |    |   ||       ||   | | |
Db     191 TTTCGGACGCCCAATTTATCCAGCAATATCTGAGTGNGAATCAGAGGAGGTTAAGGAAGG 250

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
           |    || | ||   | |||  |    | ||    ||||    |    | | || |
Db     251 CATCTCTTGTACTCACTGAGGGATTGANTGGAAGCACGCATTAACTATGTGAAGAGTAAT 310

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
           |  ||  ||| |||||||||  || ||| |  | ||||| | ||| || || || || | |
Db     311 GCGGG--TCTTTATTGTTGGGTTGAAATGGGAAGCTTGATGCCATCTTATAGTGAGAANG 368

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
           |||||||  | || ||||| || ||  | ||    ||  |  |||  || ||||| ||
Db     369 GAGAGCTTAATCTTTGGGATAAATTATTGAATGAAGCANAAATAANTGTCACTCCAGGGA 428

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTT 395
           || |   |||| |||||||| || |  ||
Db     429 TCTGCTTGTATTGCATTGAACCTGGATGGTT 459


RESULT 13
AW040322
LOCUS       AW040322                483 bp    mRNA    linear   EST 18-MAY-2001
DEFINITION  EST283186 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
            clone cLET5I3, mRNA sequence.
ACCESSION   AW040322
VERSION     AW040322.1  GI:5899076
KEYWORDS    EST.
SOURCE      tomato.
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
            Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
            Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
            ,J.
  TITLE     Generation of ESTs from tomato leaf tissue
  JOURNAL   Unpublished (1999)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Lycopersicon esculentum"
                     /cultivar="Rio Grande PtoR"
                     /db_xref="taxon:4081"
                     /clone="cLET5I3"
                     /clone_lib="tomato mixed elicitor, BTI"
                     /tissue_type="leaf"
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/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF'"
/note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2: Xhol; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
BASE COUNT 135 a 68 c 126 g 154 t
ORIGIN

Query Match 29.2%; Score 118; DB 10; Length 483;
Best Local Similarity 66.9%; Pred. No. 4.1e-29;
Matches 198; Conservative 0; Mismatches 95; Indels 3; Gaps 2;

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Qy    103 CAGCGCTTGCTCGTCGTTATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTA 162
          ||| || |  | || |  ||||| || ||  |  ||||||  |  | |  ||      |
Db      1 CAGAGCCTATTAGTTGCAATGCTTTCAGATGCTGGGTTCATCAAGGATTATATGAGAACA 60

Qy    163 AACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGG 222
          ||||||| || | |    | | |||  |    ||| |||||  ||  |  ||  ||  | ||
Db     61 AACAGAGAGAGATTGCGCAAAGTGTTTGACTTATTTGTGGCAGGTCTAAAACAAT-TGGG 119

Qy    223 CATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTG 282
          ||||  ||||| | ||||||| | ||||  || |||||  ||||    | ||||||||||
Db    120 CATCGAATGCATGAAAAGCAGTGCAGGC--CTGTATTGCTGGGTTAATATGAGCGGATTG 177

Qy    283 ATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCT 342
          ||| |  | || |  ||||| ||||||||  ||||| ||||| ||| |  | ||  | |||
Db    178 ATTGGCCCTTATAATGAAAAGGGAGAGCTTGAGCTGTGGGAGAAGCTCTTGAATGTAGCT 237

Qy    343 AAGGTAAACGTTACTCCCGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAG 398
          ||| |||||||  |||||  || ||   ||| ||||||||||||||  || |  || ||
Db    238 AAGATAAACGTGACTCCAGGGTCAGCTTGCCATTGTATTGAACCTGGATGGTTCAG 293
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RESULT 14
AV808550/c
LOCUS AV808550 423 bp mRNA linear EST 29-MAR-2002
DEFINITION AV808550 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-55-E15 3', mRNA sequence.
ACCESSION AV808550
VERSION AV808550.1 GI:19842535
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 423)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
FEATURES Location/Qualifiers
source 1. .423
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL09-55-E15"
/clone_lib="RAFL9"
/dev_stage="plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT 121 a 101 c 72 g 129 t
ORIGIN

Query Match 27.9%; Score 112.6; DB 10; Length 423;
Best Local Similarity 64.2%; Pred. No. 2.8e-27;
Matches 201; Conservative 0; Mismatches 109; Indels 3; Gaps 2;

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Qy     92 CAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCTCGGACACGCGGTTCACTCAAAAGT 151
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Db    423 CATCTCCAACCCAACATTTGCTGATATCCGCAATCTCCAATCCAAAAAATGTTCAGAGAT 364

Qy    152 TCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCGGGGGTTG 211
          |  |  |    |||||   || | |  | || || ||| | |   ||||||  |||||||
Db    363 TTGTGAAAACCAACAGGCAGAGATTGCAGAGTATCTACACGGAGCTCGTGG-AGGGGTTG 305

Qy    212 AAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGGGCCGACA 271
          ||  |  | || |||   |||||  ||||| |  |||| |||||||  | |
Db    304 AAAGAGTTAGGGATCGAGTGCACAAGAAGCAATGGAGGGT--TCTACTGTTGGGCTTATA 247

Qy    272 TGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGC 331
          || | |||||||||  ||| ||||||||||||| ||| | ||||| ||| ||||| |
Db    246 TGCGAGGATTGATTTCATCTTACAGCGAAAAAGGCGAGATTGAGCTGTGGAACAAGCTCT 187

Qy    332 TAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTTGTTGTCATTGTATTGAACCCGGCT 391
          | |||||||  ||| | || || |  || || ||||||||||| ||||| ||||| || |
Db    186 TGAACATTGGCAAGATCAATGTCATACCAGGATCTTGTTGTCACTGTATCGAACCAGGAT 127

Qy    392 ACTTTAGCCTCTG 404
            ||  |  ||||
Db    126 GGTTCCGTATCTG 114
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RESULT 15
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LOCUS AV820681 420 bp mRNA linear EST 01-APR-2002
DEFINITION AV820681 RAFL11 Arabidopsis thaliana cDNA clone RAFL11-11-L09 3', mRNA sequence.
ACCESSION AV820681
VERSION AV820681.1 GI:19862660
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 420)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web

```
          site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
          details.
FEATURES             Location/Qualifiers
     source          1. .420
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                     /db_xref="taxon:3702"
                     /clone="RAFL11-11-L09"
                     /clone_lib="RAFL11"
                     /dev_stage="plants at various developmental stages from
                     germination to mature seeds"
                     /lab_host="DH10B"
                     /note="Site_1: BamHI; Site_2: SalI; subjected to various
                     treatments (dehydration, cold, high salt, ABA, heat and UV
                     ). Dark-grown plants"
BASE COUNT      122 a    105 c     64 g    129 t
ORIGIN

  Query Match             26.5%;  Score 107.2;  DB 10;  Length 420;
  Best Local Similarity   70.7%;  Pred. No. 2e-25;
  Matches  171;  Conservative    0;  Mismatches   68;  Indels    3;  Gaps    2;

Qy     163 AACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGG 222
           |||||    || | |   | || || ||| | |    ||||||  |||||||||  |   | ||
Db     408 AACAGGCAGAGATTGCAGAGTATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGG 350

Qy     223 CATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTG 282
            |||   |||||   |||||  ||||| |  |||| |||||||| || ||| | ||||||
Db     349 GATCGAGTGCACAAGAAGCAATGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTG 292

Qy     283 ATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCT 342
           |||  ||| ||||||||||||||| ||| | ||||| ||| ||||| |  | |||||||
Db     291 ATTTCATCTTACAGCGAAAAAGGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGC 232

Qy     343 AAGGTAAACGTTACTCCCGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTC 402
           ||| | || || |  || || |||||||||| ||||| ||||| || |  ||  |  ||
Db     231 AAGATCAATGTCATACCAGGATCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATC 172

Qy     403 TG 404
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Db     171 TG 170


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Job time : 1217 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:11:12 ; Search time 43 Seconds
(without alignments)
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Title: US-09-975-842-1
Perfect score: 404
Sequence: 1 gggttgccggggttcaggat.....cccggctactttagcctctg 404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	194.8	48.2	1743	4	US-09-171-482-1	Sequence 1, Appli
	2	98.4	24.4	4459	4	US-09-363-243-2	Sequence 2, Appli
	3	98	24.3	1384	2	US-08-860-577-1	Sequence 1, Appli
	4	86.6	21.4	961	4	US-08-846-826A-3	Sequence 3, Appli
	5	84.6	20.9	968	4	US-08-846-826A-1	Sequence 1, Appli
	6	83.8	20.7	994	2	US-08-860-577-7	Sequence 7, Appli
	7	83.6	20.7	1878	1	US-08-724-194-3	Sequence 3, Appli
	8	80.4	19.9	1096	3	US-09-043-627-7	Sequence 7, Appli
	9	80.4	19.9	1113	3	US-09-043-627-9	Sequence 9, Appli
	10	78.8	19.5	1712	2	US-08-632-598-1	Sequence 1, Appli
	11	78.8	19.5	1712	4	US-09-231-240-1	Sequence 1, Appli
	12	77	19.1	1080	3	US-09-043-627-1	Sequence 1, Appli
	13	72.4	17.9	1945	1	US-08-724-194-1	Sequence 1, Appli
	14	72.4	17.9	2040	2	US-08-695-412B-11	Sequence 11, Appl
	15	72.4	17.9	2040	4	US-09-255-154D-11	Sequence 11, Appl
	16	72.4	17.9	2678	1	US-08-724-194-2	Sequence 2, Appli
	17	67.6	16.7	1703	4	US-08-378-313-18	Sequence 18, Appl
	18	64.4	15.9	1104	3	US-09-043-627-3	Sequence 3, Appli
	19	64.4	15.9	2230	4	US-08-378-313-24	Sequence 24, Appl
	20	64.4	15.9	7244	4	US-08-378-313-26	Sequence 26, Appl
	21	62.8	15.5	15397	2	US-08-673-768-1	Sequence 1, Appli
c	22	62.8	15.5	15397	2	US-08-673-768-1	Sequence 1, Appli
	23	61.6	15.2	5613	2	US-08-463-418-1	Sequence 1, Appli
	24	61.2	15.1	1800	1	US-07-809-457A-8	Sequence 8, Appli
	25	61.2	15.1	1800	1	US-08-553-943-8	Sequence 8, Appli
	26	61.2	15.1	1800	5	PCT-US91-09437-8	Sequence 8, Appli
	27	59.6	14.8	1888	1	US-08-485-107-1	Sequence 1, Appli
	28	58.4	14.5	1098	3	US-09-043-627-5	Sequence 5, Appli
	29	54.2	13.4	1497	2	US-08-860-577-11	Sequence 11, Appl
	30	48.2	11.9	7587	4	US-08-378-313-22	Sequence 22, Appl
	31	48.2	11.9	9060	4	US-08-378-313-20	Sequence 20, Appl
c	32	31.6	7.8	46819	4	US-09-453-702B-72	Sequence 72, Appl
	33	30.4	7.5	46899	1	US-08-471-119A-1	Sequence 1, Appli
c	34	29.8	7.4	1473	4	US-09-134-001C-673	Sequence 673, App
c	35	29.8	7.4	5931	3	US-08-783-774-1	Sequence 1, Appli
c	36	29.8	7.4	5931	4	US-09-556-706B-1	Sequence 1, Appli
	37	29.8	7.4	24417	2	US-08-846-762-1	Sequence 1, Appli
c	38	29.2	7.2	7218	1	US-08-232-463-14	Sequence 14, Appl
c	39	28.8	7.1	610	4	US-09-328-111-424	Sequence 424, App
	40	28.6	7.1	15393	4	US-09-453-702B-191	Sequence 191, App
	41	28.2	7.0	87563	4	US-09-453-702B-57	Sequence 57, Appl
	42	27.6	6.8	1209	4	US-08-791-115B-24	Sequence 24, Appl
	43	27.6	6.8	1962	4	US-08-791-115B-3	Sequence 3, Appli
	44	27.4	6.8	289	4	US-09-007-005-17	Sequence 17, Appl
	45	27.4	6.8	289	4	US-09-244-796-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-171-482-1
; Sequence 1, Application US/09171482A
; Patent No. 6184449
; GENERAL INFORMATION:
; APPLICANT: Ranu, Rajinder S.
; TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
; TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
; FILE REFERENCE: TAGAWA-ROSE
; CURRENT APPLICATION NUMBER: US/09/171,482A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,87
; EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect 6.1
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Rosa kardinal
US-09-171-482-1

Query Match 48.2%; Score 194.8; DB 4; Length 1743;
Best Local Similarity 71.2%; Pred. No. 5.5e-59;
Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;

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Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
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Db    1232 TTCCAGGTTTCAGGGTGGGTGCCATCTACTCCTTTAACAAGAATGTCTTGACTGCTGCTA 1291

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           |||||||||| || || || || || || || || ||  | || || |||||  ||  |||||
Db    1292 AAAAGTTGACAAGGTTCTCTTCTATCTCCGCCCCATCCCAACGGTTGCTTATCTCTATGC 1351

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | || |||||    || |  || |||||||||||| | |||||||  |  |||    |||
Db    1352 TTTCAGACACCAAATTTATGCATAAGTTCATCGAGATTAACAGAGAAAGGCTCCGTGGAA 1411

Qy     185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
           ||||   |  ||| ||| |  || |||||| || | |||||    |||||  | ||||
Db    1412 TGTATCTTAGATTTGTGAC-AGGATTGAAGCAATTGGGCATTGAGTGCACAAAGAGCAAT 1470

Qy     245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
           || ||  | |||| |||||||| ||| |||| || || ||||| || ||||| || ||||
Db    1471 GGGGG--TTTCTACTGTTGGGCAGACTTGAGTGGGTTAATTCGCTCTTACAGTGAGAAAG 1528

Qy     305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
           | ||||| ||||| ||||| | |||| | ||  | | |||| | || |||||||| || |
Db    1529 GGGAGCTTGAGCTCTGGGATAGGTTGTTGAATGTAGGTAAGCTCAATGTTACTCCTGGAT 1588

Qy     365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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Db   1589 CTTCTTGTCATTGTATTGAACCGGGATGGTTCCGGTTTTG 1628


RESULT 2
US-09-363-243-2
; Sequence 2, Application US/09363243
; Patent No. 6414221
; GENERAL INFORMATION:
;  APPLICANT:  Oetiker, Juerg H.
;  APPLICANT:  Shiu, Oi Yin
;  APPLICANT:  Yang, Shang Fa
;  APPLICANT:  Yip, Win Kin
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Transiently Activated Stress-Inducible Plant Promoters
;  FILE REFERENCE:  02307O-097000US
;  CURRENT APPLICATION NUMBER: US/09/363,243
;  CURRENT FILING DATE:  1999-07-28
;  NUMBER OF SEQ ID NOS:  16
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4459
;   TYPE: DNA
;   ORGANISM: Lycopersicon esculentum
;   FEATURE:
;   OTHER INFORMATION: 1-aminocyclopropane-1-carboxylic acid (ACC)
;   OTHER INFORMATION: synthase (ACS) LE-ACS7 gene
;   NAME/KEY: exon
;   LOCATION: (2464)..(2742)
;   NAME/KEY: intron
;   LOCATION: (2743)..(2845)
;   NAME/KEY: exon
;   LOCATION: (2846)..(3006)
;   NAME/KEY: intron
;   LOCATION: (3007)..(3102)
;   NAME/KEY: exon
;   LOCATION: (3103)..(4066)
;   NAME/KEY: CDS
;   LOCATION: join(2464..2742, 2846..3006, 3103..4066)
US-09-363-243-2

  Query Match             24.4%;  Score 98.4;  DB 4;  Length 4459;
  Best Local Similarity   56.3%;  Pred. No. 1.2e-24;
  Matches  224;  Conservative    0;  Mismatches  171;  Indels    3;  Gaps    2;

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Db    3485 GGACTTCCAGGATTTCGAGTTGGTGCCATTTATTCCAACGACGATAGGGTCGTCTCTGCA 3544

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           |||| |||  || | || |||  ||  |||||| |||  || ||   | | ||    | |
Db    3545 GCCACAAAAATGTCTAGTTTTGGATTAATTTCATCTCAAACTCAATACCTTCTTTCTGCT 3604

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
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Db    3605 TTGCTATCAGACAAAAAGTTCACGAAAAATTACGTGTCTGAAAATCAAAAGAGGCTGAAA 3664

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
           | |    | |      | || |  ||  || || ||| | || ||  | |||   || ||
Db    3665 AAACGACATGAAATGCTAGTTGGTGGTCTTAAACAAA-TTGGAATAAGGTGCCTTGAGAG 3723

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           ||  |  || |  | | ||||||||  || |||||      |  |  | ||  |||
Db    3724 CAATGCTGGGT--TGTTTTGTTGGGTGGATATGAGACATCTTTTAAGTTCAAACACATTT 3781

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           | |||||  | ||  ||||| | ||  |  |  ||   |    | ||||  || |  |
Db    3782 GATGGAGAAATGGAATTATGGAAGAAAATAGTGTACGAAGTAGGGCTAAATATTTCAGCT 3841

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAG 398
           || || |  || |||||||  ||||| || |  ||| |
Db    3842 GGATCGTCATGCCATTGTACAGAACCGGGTTGGTTTCG 3879


RESULT 3
US-08-860-577-1
; Sequence 1, Application US/08860577
; Patent No. 5998702
;  GENERAL INFORMATION:
;    APPLICANT:  Boeshore, Maury L.
;    APPLICANT:  Deng, Rosaline Z.
;    APPLICANT:  Carney, Kim J.
;    APPLICANT:  Ruttencutter, Glen E.
;    APPLICANT:  Reynolds, John F.
;    TITLE OF INVENTION:  Transgenic Plants Expressing ACC
;    TITLE OF INVENTION:  Synthase Genes
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,577
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueller, Lisa V.
;      REGISTRATION NUMBER:  38,978
;      REFERENCE/DOCKET NUMBER:  SVS3801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1384 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..39
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..433
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  595..1383
US-08-860-577-1

  Query Match             24.3%;  Score 98;  DB 2;  Length 1384;
  Best Local Similarity   55.9%;  Pred. No. 9.2e-25;
  Matches  226;  Conservative    0;  Mismatches  175;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  | || || ||  |  | ||    || ||||| |||||||| || ||  | |  ||
Db     970 GGTCTTCCCGGTTTTCGAGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA 1029

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || | || | || |||| ||  |      | ||  ||| ||| || | | || | |
Db    1030 GCGAGAAGGATGTCGAGTTTCACGCTTGTCTCGTCTCAGACACAACACATGTTGGCTTCC 1089

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||| | |||||       ||| ||  | |||| |||   | |||||  | |  |  || |
Db    1090 ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 1149

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
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Db   1150 AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG 1208

Qy    241 CAGCGGAGGCTTCTCTATTCTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300

Db   1209 TAATGCAGGGT--TGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA 1266

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360

Db   1267 CAAGGCGAGCTCGAGCTTTGGGATGTGATCTTGAAGGAACTAAAGCTGAATATATCTCCT 1326

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404

Db   1327 GGATCTTCGTGCCATTGCTCGGAGTATGGATGGTTTAGGATTTG 1370


RESULT 4
US-08-846-826A-3
; Sequence 3, Application US/08846826A
; Patent No. 6194639
;  GENERAL INFORMATION:
;    APPLICANT:  Botella, Jose
;    APPLICANT:  Sanewski, Garth
;    TITLE OF INVENTION:  NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  One Commerce Square, 2005 Market Street, 22nd
;      STREET:  Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,826A
;      FILING DATE:  01-MAY-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN9582
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nadel Esq., Alan S.
;      REGISTRATION NUMBER:  27,363
;      REFERENCE/DOCKET NUMBER:  8795-11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1280
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  961 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..102
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  103..194
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  195..961
US-08-846-826A-3

  Query Match             21.4%;  Score 86.6;  DB 4;  Length 961;
  Best Local Similarity   55.9%;  Pred. No. 8.4e-21;
  Matches  205;  Conservative    0;  Mismatches  159;  Indels    3;  Gaps    2;

Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60

Db    567 GGGCTACCAGGCTTTCGCGTCGGTGCGATACACTCCCAAAATGAGGCGGTGGTCTCCACG 626

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120

Db    627 GCGACCAAGATGTCGAGCTTTGGGCTCATCTCCTCTCAAACTCAGTACTTCTTGTCCTTG 686

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180

Db    687 TTGCTCTCCGACAAGGAGTTCACAGCGAACTACATAGCGGAGAACAAGAAGCGGCT-TAG 745

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240

Db    746 AGAGCGGCAAAAGCGGCTCACCGAAGCGCTGCGGACGATCGGTATAAACTGTTTGGAGAG 805

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300

Db    806 CAATGCAGGGT--TGTTTTGTTGGGTGGACATGAGGCACTTACTTAAGTCTAAGACACCT 863

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360

Db    864 GAAGGAGAGATGGAGCTGTGGAAAAGGATAGTGCATGATGTGGGACTAAACATTTCTCCG 923

Qy    361 GGTTCTT 367

Db    924 GGCTCTT 930


RESULT 5
US-08-846-826A-1
; Sequence 1, Application US/08846826A
; Patent No. 6194639
;  GENERAL INFORMATION:
;    APPLICANT:  Botella, Jose
;    APPLICANT:  Sanewski, Garth
;    TITLE OF INVENTION:  NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  One Commerce Square, 2005 Market Street, 22nd
;      STREET:  Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,826A
;      FILING DATE:  01-MAY-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN9582
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nadel Esq., Alan S.
;      REGISTRATION NUMBER:  27,363
;      REFERENCE/DOCKET NUMBER:  8795-11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1280
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  968 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..968
US-08-846-826A-1

  Query Match             20.9%;  Score 84.6;  DB 4;  Length 968;
  Best Local Similarity   52.7%;  Pred. No. 4.3e-20;
  Matches  208;  Conservative    0;  Mismatches  184;  Indels    3;  Gaps    1;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     571 GGCCTCCCCGGTTTTAGGGTTGGGACGATCTATTCATACAACAATAGGGTGGTGACCACG 630

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     631 GCGAGGAGGATGTCGAGCTTCACACTCGTGTCGTCGCAGACTCAGAAGACGCTGGCGTCG 690

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     691 ATGCTGTCGGACGAGGAGTTCACAAAGTACTACATAAGGACCAACAGGGAGAGGCTGAAG 750

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     751 AGGAGGTACGAGTACATAATCCAGGGGCTGGAGAGAGCAGGGATTGAGTGCTTCCAAGGG 810

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     811 AATGCCGGGCTGTTC---TGCTGGATGAATCTGGGGCCACTCCTGGAGGAGCAGACGAGA 867

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     868 GAAGGGGAGCTCAGCCTGTGGAAACTGATATTGCATGAGGTGAGGCTCAACATATCACCA 927

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTT 395
Db     928 GGATCTTCATGCCACTGCTCTGAGCCTGGCTGGTT 962


RESULT 6
US-08-860-577-7
; Sequence 7, Application US/08860577
; Patent No. 5998702
;  GENERAL INFORMATION:
;    APPLICANT:  Boeshore, Maury L.
;    APPLICANT:  Deng, Rosaline Z.
;    APPLICANT:  Carney, Kim J.
;    APPLICANT:  Ruttencutter, Glen E.
;    APPLICANT:  Reynolds, John F.
;    TITLE OF INVENTION:  Transgenic Plants Expressing ACC
;    TITLE OF INVENTION:  Synthase Genes
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,577
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueller, Lisa V.
;      REGISTRATION NUMBER:  38,978
;      REFERENCE/DOCKET NUMBER:  SVS3801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..975
US-08-860-577-7

  Query Match             20.7%;  Score 83.8;  DB 2;  Length 994;
  Best Local Similarity   55.3%;  Pred. No. 8.3e-20;
  Matches  204;  Conservative    0;  Mismatches  162;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     621 GGTCTTCCCGGTTTTCGAGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA 680

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     681 GCGAGAAGGATGTCGAGTTTCACGCTTGTCTCGTCTCAGACACAACACATGTTGGCTTCC 740

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     741 ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 800

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     801 AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG 859

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     860 TAATGCAGG--TTTGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA 917

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     918 CAAGGCGAGCTCGAGCTTTGGGATGTGATCTTGGAGGAACTAAAGCTGAATATATCTCCT 977

Qy     361 GGTTCTTGT 369
Db     978 GATCTTCGT 986


RESULT 7
US-08-724-194-3
; Sequence 3, Application US/08724194
; Patent No. 5824875
;  GENERAL INFORMATION:
;    APPLICANT:  RANU, RAJINDER S.
;    TITLE OF INVENTION:  ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
;    TITLE OF INVENTION:  SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
;    TITLE OF INVENTION:  IN GERANIUMS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SANTANGELO LAW OFFICES PC
;      STREET:  315 WEST OAK STREET, STE 701
;      CITY:  FORT COLLINS
;      STATE:  CO
;      COUNTRY:  USA
;      ZIP:  80521
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,194
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;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SANTANGELO, LUKE
;      REGISTRATION NUMBER:  31,997
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (970) 224-3100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1878 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-724-194-3

  Query Match             20.7%;  Score 83.6;  DB 1;  Length 1878;
  Best Local Similarity   53.7%;  Pred. No. 1.4e-19;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     953 GGCTTCCCTGGCTTCAGGGTGGGGATTGTCTACTCCTACAATGACGCAGTTGTGAATTGT 1012

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db   1013 GCGCGAAAGATGTCAAGTTTCGGCCTTGTATCCACACAAACTCAGCACCTAATCGCATCA 1072

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db   1073 ATGCTCTCGGACGATGAATTCGTGGACACATTCATCGTGGAGAGCGCGAAGAGGCTAGCG 1132

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db   1133 AGAAGGTACACAACCTTCACAAGAGGGCTTGCA-CAAGTGAACATTGGATGCCTAAAGAG 1191

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db   1192 CAATGGGGGGTTATTCAT--ATGGATGGACTTGAGGAGGCTTCTCAAGGAGAAGACTTTC 1249

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db   1250 GAGGCGGAGATGGCTCTGTGGAGAGTGATAATCAATGAAGTGAAGCTAAATGTGTCGCCA 1309

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db   1310 GGGGCGTCGTTCCATTGCTCGGAGCCAGGGTGGTTTAGAGTGTG 1353


RESULT 8
US-09-043-627-7
; Sequence 7, Application US/09043627
; Patent No. 6124525
;  GENERAL INFORMATION:
;    APPLICANT:  Botella, Jose Ramon
;    TITLE OF INVENTION:  NOVEL ACC SYNTHASE GENES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
;      STREET:  100 Thanet Circle, Suite 306
;      CITY:  Princeton
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08540-3662
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/043,627
;      FILING DATE:  20-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU96/00591
;      FILING DATE:  20-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN5559
;      FILING DATE:  20-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN9603
;      FILING DATE:  02-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bernstein, Scott N.
;      REGISTRATION NUMBER:  38,827
;      REFERENCE/DOCKET NUMBER:  3573-11US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-924-8555
;      TELEFAX:  609-924-3036
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1096 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1095
US-09-043-627-7

  Query Match             19.9%;  Score 80.4;  DB 3;  Length 1096;
  Best Local Similarity   53.2%;  Pred. No. 1.4e-18;
  Matches  215;  Conservative    0;  Mismatches  186;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db     688 GGCCTCCCTGGCTTTAGGGTTGGCATTGTTTATTCTTATAATGATGCAGTTGTGAGTTGT 747

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db     748 ATCCGCAAGATGTCAAGCTTCGGTTTGGTATCCTCACAAACTCAATATTTACTCGCTTCA 807

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db     808 ATGCTTTCTGATGATGAATTTGTGGAAAAGTTTCTAGCGGAAAGCTCAAAGAGGCTGGCA 867

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db     868 AAAAGGTACCATATTTTCACAAAGAGACTTG-AGAAAGTGGGGATTAACTGCTTGAAGGG 926

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db     927 AAATGCAGG--TCTTTTCTTCTGGATGGATTTGCGACACCTCCTTCAACAAGAAACAGTT 984

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db     985 GATGCCGAAATGAAGCTATGGGGCACGATTTTGAACGATGTGAAACTTAACGTTTCACCA 1044

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1045 GGCTCTTCCTTTCATTGCCAGGAGCCTGGTTGGTTCAGAGTCTG 1088


RESULT 9
US-09-043-627-9
; Sequence 9, Application US/09043627
; Patent No. 6124525
;  GENERAL INFORMATION:
;    APPLICANT:  Botella, Jose Ramon
;    TITLE OF INVENTION:  NOVEL ACC SYNTHASE GENES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
;      STREET:  100 Thanet Circle, Suite 306
;      CITY:  Princeton
```

```
;       STATE:  NJ
;       COUNTRY:  USA
;       ZIP:  08540-3662
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/043,627
;       FILING DATE:  20-MAR-1998
;       CLASSIFICATION:  800
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/AU96/00591
;       FILING DATE:  20-SEP-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  AU PN5559
;       FILING DATE:  20-SEP-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  AU PN9603
;       FILING DATE:  02-MAY-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bernstein, Scott N.
;       REGISTRATION NUMBER:  38,827
;       REFERENCE/DOCKET NUMBER:  3573-11US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  609-924-8555
;       TELEFAX:  609-924-3036
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1113 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1113
US-09-043-627-9

  Query Match             19.9%;  Score 80.4;  DB 3;  Length 1113;
  Best Local Similarity   53.2%;  Pred. No. 1.4e-18;
  Matches  215;  Conservative    0;  Mismatches  186;  Indels    3;  Gaps    2;

Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
          ||||| || || || ||| | ||| |||| ||||| |||||||| |  ||  | | |
Db    694 GGGTTCCCAGGCTTTAGGGTCGGCATTATATACTCATACAACGATACAGTTGTGAGTTGC 753

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          |||   ||  || | || |||  |    | ||| | |  || || |  ||  |||
Db    754 GCCTGCAAAATGTCAAGCTTTGGACTTGTATCATCACAAACTCAACATTTAATCGCTTCA 813

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||| | || ||       ||     | | ||||||    |  |        |  ||   |
Db    814 ATGTTATCAGATGATGAATTTGTGGATAGGTTCATTACTGAGAGTGCTAAAAGGCTTGCA 873

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
          | || | ||   || |||     ||||| |     || | |||||  | ||   | | ||
Db    874 AAAAGGCACAGAGCCTTC-ACATGGGGGCTATCTCAAGTAGGCATTGGTTGTTTGAAGAG 932

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          ||  |  ||   || | ||  |||   ||  ||       |  |        | |  ||
Db    933 CAATGCGGG--GCTATTTTTCTGGATGGATTTGCATCATCTCCTCAAGGAGCAAACTGAT 990

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           ||| |||| | || || ||| |   | |  | |||   | |||  |||| ||| ||||
Db    991 GAAGCAGAGATAGAACTGTGGAAAGTGATAATCAACGAAGTTAAATTAAATGTTTCTCCG 1050

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          |||||||  | ||||||   | | || || |  ||| |  | ||
Db   1051 GGTTCTTCCTTTCATTGCGCTAATCCAGGATGGTTTCGGGTTTG 1094
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RESULT 10
US-08-632-598-1
; Sequence 1, Application US/08632598
; Patent No. 5886164
;  GENERAL INFORMATION:
;    APPLICANT:  BIRD, COLIN R
;    APPLICANT:  FLETCHER, JONATHON D
;    TITLE OF INVENTION:  RIPENING-RELATED GENES FROM BANANA
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY AND CUSHMAN
;      STREET:  1100 NEW YORK AVENUE N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,598
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOKULIS, PAUL N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  223355/SEE50112/US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  861-3000
;      TELEFAX:  822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1712 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  MUSA
;    IMMEDIATE SOURCE:
;      CLONE:  ACS GENE
US-08-632-598-1

  Query Match             19.5%;  Score 78.8;  DB 2;  Length 1712;
  Best Local Similarity   53.0%;  Pred. No. 6.5e-18;
  Matches  214;  Conservative    0;  Mismatches  187;  Indels    3;  Gaps    2;

Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
          ||  | || || ||| |  | ||||| || ||||||||||||||   |||| |||
Db    865 GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          || |  ||| || |||| |||  |    | ||  | | ||||||| | ||||||
Db    925 GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||| |    |||  |  ||||||    |  ||| | | |   | | |  |||   |
Db    985 ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
            |  |  |   |  ||   ||   ||  | ||| | |||| || |  |||  ||| |
Db   1045 GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          || ||  ||   || |  || |||   ||| ||||    ||| |           | |
Db   1104 CAACGCGGG--GCTGTTCTGCTGGATGGACTTGAGGCCGTTGCTGAAGGAAGCGACGGTG 1161

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           | |  ||  ||  ||| |||     | |  | |||   |  ||| | ||| |  | ||
Db   1162 GAGGCGGACGTCCGGCTGTGGCGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG 1221
```

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Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || |  |  || ||    || || || |  || ||  | ||
Db    1222 GGGTCGTCCTTCCACTGCTCGGAGCCGGGGTGGTTCAGGGTGTG 1265


RESULT 11
US-09-231-240-1
; Sequence 1, Application US/09231240
; Patent No. 6262346
;  GENERAL INFORMATION:
;    APPLICANT:  BIRD, COLIN R
;    APPLICANT:  FLETCHER, JONATHON D
;    TITLE OF INVENTION:  RIPENING-RELATED GENES FROM BANANA
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY AND CUSHMAN
;      STREET:  1100 NEW YORK AVENUE N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/231,240
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,598
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOKULIS, PAUL N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  223355/SEE50112/US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  861-3000
;      TELEFAX:  822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1712 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  MUSA
;    IMMEDIATE SOURCE:
;      CLONE:  ACS GENE
US-09-231-240-1

  Query Match             19.5%;  Score 78.8;  DB 4;  Length 1712;
  Best Local Similarity   53.0%;  Pred. No. 6.5e-18;
  Matches  214;  Conservative    0;  Mismatches  187;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
             ||  | || || ||| |  | ||||| || ||||||||||||||   |||| |||
Db     865 GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || |  ||| || |||| |||  |    | ||  | | |||||||| | ||||||
Db     925 GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||| |    |||  |  ||||||    |  ||| | | |   | | |  |||   |
Db     985 ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             |  | |  |  ||  ||  ||  | |||  | |||| || |  |||  |||  |

Db    1045 GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
           || ||  ||   || |  || |||   ||| ||||    ||| |         |  |
Db    1104 CAACGCGGG--GCTGTTCTGCTGGATGGACTTGAGGCCGTTGCTGAAGGAAGCGACGGTG 1161

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           | |  ||  ||  ||| |||     | |  | |||   |  ||| | ||| |  | ||
Db    1162 GAGGCGGACGTCCGGCTGTGGCGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG 1221

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           || || |  |  || ||    || || || |  || ||  | ||
Db    1222 GGGTCGTCCTTCCACTGCTCGGAGCCGGGGTGGTTCAGGGTGTG 1265


RESULT 12
US-09-043-627-1
; Sequence 1, Application US/09043627
; Patent No. 6124525
;  GENERAL INFORMATION:
;    APPLICANT:  Botella, Jose Ramon
;    TITLE OF INVENTION:  NOVEL ACC SYNTHASE GENES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
;      STREET:  100 Thanet Circle, Suite 306
;      CITY:  Princeton
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08540-3662
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/043,627
;      FILING DATE:  20-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU96/00591
;      FILING DATE:  20-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN5559
;      FILING DATE:  20-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PN9603
;      FILING DATE:  02-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bernstein, Scott N.
;      REGISTRATION NUMBER:  38,827
;      REFERENCE/DOCKET NUMBER:  3573-11US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-924-8555
;      TELEFAX:  609-924-3036
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1080 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1080
US-09-043-627-1

  Query Match             19.1%;  Score 77;  DB 3;  Length 1080;
  Best Local Similarity   53.2%;  Pred. No. 2.2e-17;
  Matches  208;  Conservative    0;  Mismatches  180;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
             ||  | || || ||| |  | ||  |  | || ||||||||||| |  ||| | | |
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Db    691 GGTCTCCCCGGATTCCGAGTCGGGATCGTGTATTCCTACAACGACACGGTGGTTAGTTGC 750

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          ||    |   || |||| ||       | | ||  | | ||| |||  | | || | ||
Db    751 GCACGCAGAATGTCGAGCTTCGGCCTCGTCTCGTCGCAGACACAGTACCTACTGGCCGCC 810

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||||| || | |       ||    | ||  ||  |     | || |      ||  ||
Db    811 ATGCTATCCGGCGAAGAATTTTTGCCAACATTACTGACTGAAAGCGCGAAGAGTCTGTCG 870

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
            |   ||      |||    | ||  |||| |||  ||| |||||| |||  |||  |
Db    871 GAGAGCCACAGGATCTTCTCTTCCGGCCTTGAGGAAG-TCGACATCCGCTGCTTGGACGG 929

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          ||  |  ||    |||  || |||   ||| |  |     |  |   |     || ||||
Db    930 CAATGCCGGGG--TCTTCTGCTGGATGGACCTACGGCACCTCCTCAAAGAAGCCACCGAA 987

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            | || ||||||||||| |||  |  | |  | |||| ||  ||| | || ||  | |||
Db    988 GACGGCGAGCTCGAGCTGTGGCGCGTGATAGTGAACAATGTCAAGCTCAATGTGTCCCCC 1047

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCT 391
          |||||  |  | | ||||    || || || |
Db   1048 GGTTCGTCGTTTTATTGCGCCGAGCCAGGTT 1078
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RESULT 13
US-08-724-194-1
; Sequence 1, Application US/08724194
; Patent No. 5824875
; GENERAL INFORMATION:
; APPLICANT: RANU, RAJINDER S.
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
; TITLE OF INVENTION: IN GERANIUMS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANTANGELO LAW OFFICES PC
; STREET: 315 WEST OAK STREET, STE 701
; CITY: FORT COLLINS
; STATE: CO
; COUNTRY: USA
; ZIP: 80521
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,194
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTANGELO, LUKE
; REGISTRATION NUMBER: 31,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 224-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-724-194-1

Query Match 17.9%; Score 72.4; DB 1; Length 1945;
Best Local Similarity 53.7%; Pred. No. 1.3e-15;
Matches 217; Conservative 0; Mismatches 181; Indels 6; Gaps 3;

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Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
            ||  |||| |||||| |  | ||  |  | ||||| | ||||||  |||| |  |
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Db    918 GGCATGCCCGGGTTCCGCGTCGGGATCGTGTACTCATTCAACGACGACGTCGTATCCTGC 977

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          ||    ||| || |||| ||    |   | ||  | | |||||||| | | ||||  |
Db    978 GCACGGAAGATGTCGAGCTTCGGGTTGGTGTCGACCCAGACGCAGCACCTTCTCGCAGCG 1037

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||||| || |||      |||    |   |||| ||| ||   | ||   ||   |
Db   1038 ATGCTATCCGACGACGTTTTCGTGGAGCGGTTCCTCGCGG---AGAGCCGGAGCTTGGGG 1094

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
          || | | |||  |  |||  |   ||| | | || |  | || ||  | ||     | ||
Db   1095 AGGAGGCACGGCGTGTTCACGAAAGGGCTCG-AGGAGTTGGGGATTGGGTGTTTAAAGAG 1153

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          || ||  ||   ||||| |  |||   ||  || |     |  |   |  | |
Db   1154 CAACGCGGG--GCTCTACTTCTGGATGGATTTGCGGAAGCTTCTAGAAGAAGAGACGTTT 1211

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
            | |  ||| | | ||| ||| |    | |  | ||    |  ||| |||||||  ||||
Db   1212 GAGGCGGAGATGGTGCTGTGGAAGGTGATTATTAATGAGGTGAAGCTAAACGTGTCTCCG 1271

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          || || |  | ||||||  | || || || |  |||||  | ||
Db   1272 GGGTCGTCGTTTCATTGCGTGGAGCCGGGTTGGTTTAGGGTTTG 1315
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RESULT 14
US-08-695-412B-11
; Sequence 11, Application US/08695412B
; Patent No. 5874269
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: MOISYADI, STEFAN
; APPLICANT: NEUPANE, KABI R.
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
; TITLE OF INVENTION: RIPENING OF COFFEE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JONES, DAY, REAVIS & POGUE
; STREET: NORTH POINT, 901 LAKESIDE AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v. 5.1
; SOFTWARE: WordPerfect v. 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,412B
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/485,107
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRIFFITH, CALVIN P.
; REGISTRATION NUMBER: 34,831
; REFERENCE/DOCKET NUMBER: 265036600002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 586-7050
; TELEFAX: (216) 579-0212
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2040 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

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;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  178..1653
US-08-695-412B-11

  Query Match            17.9%;  Score 72.4;  DB 2;  Length 2040;
  Best Local Similarity   52.0%;  Pred. No. 1.3e-15;
  Matches  210;  Conservative    0;  Mismatches  191;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db    1027 GGCTTCCCTGGATTCAGAGTTGGCATTTTGTATTCATATAATGACGCTGTTGTCAGCTGT 1086

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db    1087 GCTAGAAAAATGTCGAGTTTCGGCCTTGTTTCAACACAAACTCAGCATCTGATTGCATCA 1146

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db    1147 ATGTTATCGGACGAAGCATTTATGGACAAAATCATTTCCACGAGCTCAGAGAGATTAGCT 1206

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db    1207 GCAAGGCATGGTCTTTTCACAAGAGGACTTG-CTCAAGTAGGCATTGGCACCTTAAAAAG 1265

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db    1266 CAGTGCGGGC--CTTTATTTCTGGATGGACTTAAGGAGACTCCTCAGGGAGTCCACATTT 1323

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db    1324 GAGGCAGAAATGGAACTTTGGAGGATCATAATACATGAAGTCAAGCTCAATGTTTCACCA 1383

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1384 GGCTTATCTTTCCATTGCTCAGAACCAGGATGGTTCAGAGTTTG 1427


RESULT 15
US-09-255-154D-11
; Sequence 11, Application US/09255154D
; Patent No. 6448474
;  GENERAL INFORMATION:
;       APPLICANT: STILES, JOHN I.
;                  MOISYADI, ISTEFO
;                  NEUPANE, KABI R.
;       TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
;                           DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
;                           RIPENING OF COFFEE
;       NUMBER OF SEQUENCES: 21
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: JONES, DAY, REAVIS & POGUE
;            STREET: NORTH POINT, 901 LAKESIDE AVENUE
;            CITY: CLEVELAND
;            STATE: OHIO
;            COUNTRY: USA
;            ZIP: 44114
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;                         storage
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: MS-DOS v. 5.1
;            SOFTWARE: WordPerfect v. 6.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/255,154D
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/695,412
;            FILING DATE: 12-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: GRIFFITH, CALVIN P.
;            REGISTRATION NUMBER: 34,831
;            REFERENCE/DOCKET NUMBER: 265036600002
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (216) 586-7050
;            TELEFAX: (216) 579-0212
;  INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2040 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA to mRNA
;       FEATURE:
;            NAME/KEY: CDS
;            LOCATION: 178..1653
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-255-154D-11

  Query Match            17.9%;  Score 72.4;  DB 4;  Length 2040;
  Best Local Similarity   52.0%;  Pred. No. 1.3e-15;
  Matches  210;  Conservative    0;  Mismatches  191;  Indels    3;  Gaps    2;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
Db    1027 GGCTTCCCTGGATTCAGAGTTGGCATTTTGTATTCATATAATGACGCTGTTGTCAGCTGT 1086

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
Db    1087 GCTAGAAAAATGTCGAGTTTCGGCCTTGTTTCAACACAAACTCAGCATCTGATTGCATCA 1146

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
Db    1147 ATGTTATCGGACGAAGCATTTATGGACAAAATCATTTCCACGAGCTCAGAGAGATTAGCT 1206

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
Db    1207 GCAAGGCATGGTCTTTTCACAAGAGGACTTG-CTCAAGTAGGCATTGGCACCTTAAAAAG 1265

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
Db    1266 CAGTGCGGGC--CTTTATTTCTGGATGGACTTAAGGAGACTCCTCAGGGAGTCCACATTT 1323

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
Db    1324 GAGGCAGAAATGGAACTTTGGAGGATCATAATACATGAAGTCAAGCTCAATGTTTCACCA 1383

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
Db    1384 GGCTTATCTTTCCATTGCTCAGAACCAGGATGGTTCAGAGTTTG 1427


Search completed: March 11, 2003, 01:19:55
Job time : 48 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:52:12 ; Search time 61 Seconds
(without alignments)
4423.601 Million cell updates/sec

Title: US-09-975-842-1
Perfect score: 404
Sequence: 1 gggttgccggggttcaggat.....cccggctactttagcctctg 404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 333959956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		194.8	48.2	1743	10	US-09-776-529A-1	Sequence 1, Appli
2	c	107.6	26.6	748	10	US-09-770-149-16	Sequence 16, Appl
3		107.6	26.6	1344	9	US-09-938-842A-1571	Sequence 1571, Ap
4		53.6	13.3	1488	9	US-09-938-842A-1726	Sequence 1726, Ap
5	c	31.6	7.8	46819	9	US-10-114-170-72	Sequence 72, Appl
6		30.4	7.5	1416	9	US-09-938-842A-583	Sequence 583, App
7	c	30.2	7.5	2302	10	US-09-920-300A-1711	Sequence 1711, Ap
8	c	30.2	7.5	2302	12	US-10-033-528-1711	Sequence 1711, Ap
9	c	30.2	7.5	7960	10	US-09-764-869-2327	Sequence 2327, Ap
10	c	30.2	7.5	17239	10	US-09-764-869-2326	Sequence 2326, Ap
11		30	7.4	353	10	US-09-924-035A-68	Sequence 68, Appl
12		29.8	7.4	398	9	US-09-954-531-90	Sequence 90, Appl
13		29.8	7.4	398	9	US-09-954-531-291	Sequence 291, App
14		29.8	7.4	398	9	US-09-954-531-508	Sequence 508, App
15		29.8	7.4	398	10	US-09-962-436-152	Sequence 152, App
16		29.8	7.4	398	10	US-09-880-107-1211	Sequence 1211, Ap
17	c	29.8	7.4	1113	9	US-09-738-626-3191	Sequence 3191, Ap
18	c	29.8	7.4	3309400	9	US-09-738-626-1	Sequence 1, Appli
19		29.4	7.3	13819	10	US-09-764-877-2596	Sequence 2596, Ap
20	c	28.8	7.1	610	10	US-09-879-536-424	Sequence 424, App
21	c	28.8	7.1	2673	9	US-09-938-842A-1853	Sequence 1853, Ap
22	c	28.8	7.1	2673	10	US-09-887-576-667	Sequence 667, App
23		28.6	7.1	2116	9	US-10-023-896-31	Sequence 31, Appl
24		28.6	7.1	2116	10	US-09-925-297-261	Sequence 261, App
25	c	28.6	7.1	2911	9	US-09-969-384-12	Sequence 12, Appl
26	c	28.6	7.1	2920	9	US-09-969-384-2	Sequence 2, Appli
27		28.6	7.1	15393	9	US-10-114-170-191	Sequence 191, App
28		28.4	7.0	1050	10	US-09-804-551B-3	Sequence 3, Appli
29		28.4	7.0	1610	9	US-10-170-656-4	Sequence 4, Appli
30		28.2	7.0	87563	9	US-10-114-170-57	Sequence 57, Appl
31		27.8	6.9	13821	10	US-09-764-877-2595	Sequence 2595, Ap
32	c	27.6	6.8	401	9	US-09-946-807-1194	Sequence 1194, Ap
33	c	27.6	6.8	401	10	US-09-795-668-1194	Sequence 1194, Ap
34	c	27.6	6.8	401	10	US-09-795-686-1194	Sequence 1194, Ap
35		27.6	6.8	1260	10	US-09-870-379-1	Sequence 1, Appli
36	c	27.6	6.8	2730	10	US-09-822-849A-248	Sequence 248, App
37	c	27.6	6.8	1503841	9	US-09-946-807-1	Sequence 1, Appli
38	c	27.6	6.8	1503841	10	US-09-795-668-1	Sequence 1, Appli
39	c	27.6	6.8	1503841	10	US-09-795-686-1	Sequence 1, Appli
40	c	27.4	6.8	519	10	US-09-780-717-51	Sequence 51, Appl
41	c	27.4	6.8	673	10	US-09-780-717-49	Sequence 49, Appl
42	c	27.4	6.8	1257	9	US-09-738-626-3137	Sequence 3137, Ap
43	c	27.4	6.8	1935	10	US-09-974-300-665	Sequence 665, App
44		27.2	6.7	170834	10	US-09-835-232-7	Sequence 7, Appli
45	c	27	6.7	346	10	US-09-867-701-7740	Sequence 7740, Ap

ALIGNMENTS

RESULT 1
US-09-776-529A-1
; Sequence 1, Application US/09776529A
; Patent No. US20020083484A1
; GENERAL INFORMATION:
; APPLICANT: Tagawa Greenhouses, Inc.
; APPLICANT: Ranu, Rajinder S.
; TITLE OF INVENTION: A 1-Aminocyclopropane-1-Carboxylate Synthase Gene From Rosa to
; TITLE OF INVENTION: Ethylene Levels In Roses
; FILE REFERENCE: Tagawa-Rose
; CURRENT APPLICATION NUMBER: US/09/776,529A
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 08/724,194
; PRIOR FILING DATE: 1996-10-01
; PRIOR APPLICATION NUMBER: US 09/171,482
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: PCT/US97/17644
; PRIOR FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Rosa kerdinal
US-09-776-529A-1

Query Match 48.2%; Score 194.8; DB 10; Length 1743;
Best Local Similarity 71.2%; Pred. No. 2.5e-57;
Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;

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Qy       5 TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
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Db    1232 TTCCAGGTTTCAGGGTGGGTGCCATCTACTCCTTTAACAAGAATGTCTTGACTGCTGCTA 1291

Qy      65 AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
           |||||||||| || || || || || || || ||  | || || ||||  ||  |||||
Db    1292 AAAAGTTGACAAGGTTCTCTTCTATCTCCGCCCCATCCCAACGGTTGCTTATCTCTATGC 1351

Qy     125 TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
           | || |||||    || |  || ||||||||||| | |||||||  |  |||    |||
Db    1352 TTTCAGACACCAAATTTATGCATAAGTTCATCGAGATTAACAGAGAAAGGCTCCGTGGAA 1411
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Qy    185 TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
          ||||   |  ||| ||| |  || |||||| || | |||||    |||||  | ||||
Db   1412 TGTATCTTAGATTTGTGAC-AGGATTGAAGCAATTGGGCATTGAGTGCACAAAGAGCAAT 1470

Qy    245 GGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAG 304
          || ||  | |||| |||||||| ||| |||| || || ||||| || ||||| || ||||
Db   1471 GGGGG--TTTCTACTGTTGGGCAGACTTGAGTGGGTTAATTCGCTCTTACAGTGAGAAAG 1528

Qy    305 GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 364
          | ||||| ||||| ||||| | |||| | ||  | | |||| | || ||||||| || |
Db   1529 GGGAGCTTGAGCTCTGGGATAGGTTGTTGAATGTAGGTAAGCTCAATGTTACTCCTGGAT 1588

Qy    365 CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          ||| ||||||||||||||||| || |  ||  |  | ||
Db   1589 CTTCTTGTCATTGTATTGAACCGGGATGGTTCCGGTTTTG 1628
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RESULT 2
US-09-770-149-16/c
; Sequence 16, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(748)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-16

Query Match 26.6%; Score 107.6; DB 10; Length 748;
Best Local Similarity 57.4%; Pred. No. 3.1e-27;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;

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Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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Db    617 GGTCTTCCTGGTTTCCGCGTGGGAACTATATACTCGTACAACGATAATGTTGTTCGGACA 558

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          || | || | || |||| ||  |     | ||  ||| ||| || |  |||| |    |
Db    557 GCGAGAAGGATGTCGAGCTTCACGCTTGTCTCGTCTCAGACACAACATATGCTGGCTTCT 498

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||| | |||||   |  ||| ||  | |||| |||   | ||||| | |  | ||| | |
Db    497 ATGTTGTCGGATGAGGAGTTTACGGAGAAGTACATTAGGATAAACCGGGAAAGACTTAGA 438

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
          |||  ||||| | |  | |||  ||| || |||||    || ||    ||   | || |
Db    437 AGACGGTACGATACCATTGTGGAAGGGCTT-AAGAAGGCAGGGATTGAGTGTTTGAAAGG 379

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          | || |||   || | |||||||    |  || |   ||| |   |   | |   ||
Db    378 GAACGCAGG--GCTATTTTGTTGGATGAATTTGGGTTTCTTGCTCGAAAAGAAAACTAAA 321

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
          | || |||||| |||| |||||   | |  ||||       ||  | ||  |  ||||
Db    320 GACGGCGAGCTCCAGCTTTGGGATGTGATCTTAAAGGAGCTGAACCTGAATATATCTCCG 261

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          || ||||  || || ||    ||  ||| |  |||||  | ||
Db    260 GGATCTTCGTGCCACTGCTCGGAGGTCGGATGGTTTAGGGTTTG 217
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RESULT 3
US-09-938-842A-1571
; Sequence 1571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1571
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1571

Query Match 26.6%; Score 107.6; DB 9; Length 1344;
Best Local Similarity 57.4%; Pred. No. 4.2e-27;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;

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Qy      1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
          ||  | || || ||| |  ||||   ||| ||||| |||||||| || ||  |    ||
Db    862 GGTCTTCCTGGTTTCCGCGTGGGAACTATATACTCGTACAACGATAATGTTGTTCGGACA 921

Qy     61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
          || | || | || |||| ||  |     | ||  ||| ||| || |  |||| |    |
Db    922 GCGAGAAGGATGTCGAGCTTCACGCTTGTCTCGTCTCAGACACAACATATGCTGGCTTCT 981

Qy    121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
          ||| | |||||   |  ||| ||  | |||| |||   | ||||| | |  | ||| | |
Db    982 ATGTTGTCGGATGAGGAGTTTACGGAGAAGTACATTAGGATAAACCGGGAAAGACTTAGA 1041

Qy    181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
          |||  ||||| | |  | |||  ||| || |||||    || ||    ||   | || |
Db   1042 AGACGGTACGATACCATTGTGGAAGGGCTT-AAGAAGGCAGGGATTGAGTGTTTGAAAGG 1100

Qy    241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
          | || |||   || | |||||||    |  || |   ||| |   |   | |   ||
Db   1101 GAACGCAGG--GCTATTTTGTTGGATGAATTTGGGTTTCTTGCTCGAAAAGAAAACTAAA 1158

Qy    301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
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Db   1159 GACGGCGAGCTCCAGCTTTGGGATGTGATCTTAAAGGAGCTGAACCTGAATATATCTCCG 1218

Qy    361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
          || ||||  || || ||    ||   ||| |  ||||  | ||
Db   1219 GGATCTTCGTGCCACTGCTCGGAGGTCGGATGGTTTAGGGTTTG 1262


RESULT 4
US-09-938-842A-1726
; Sequence 1726, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1726
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-1726

  Query Match             13.3%;  Score 53.6;  DB 9;  Length 1488;
  Best Local Similarity   47.5%;  Pred. No. 2.5e-08;
  Matches  192;  Conservative    0;  Mismatches  209;  Indels    3;  Gaps    1;

Qy       1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
           ||  |||| || || ||  | ||  |  | ||||| ||||| || |  ||| |    |
Db     847 GGTCTGCCTGGTTTAAGAGTTGGTATAGTATACTCTTACAATGACAGGGTGGTTCAGATC 906

Qy      61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
           || |  ||  || |||| ||        ||||  | |  ||||||  ||| |||
Db     907 GCAAGGAAAATGTCGAGTTTCGGTCTTGTTTCGTCACAAACGCAGCATTTGATCGCTAAA 966

Qy     121 ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
           ||| | || ||      |||     |  |||| |||   |  | || |  |    |
Db     967 ATGTTATCCGATGAAGAGTTTGTAGACGAGTTTATCCGCGAGAGCAAATTGCGGTTAGCT 1026

Qy     181 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
             || | ||||||   |     | ||  | || |      ||  |      |     ||||
Db    1027 GCAAGGCACGCTGAGATAACCACCGGTTTAGATGGTTTAGGGATTGGTTGGTT---AAAG 1083

Qy     241 CAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAA 300
                   | |  |  | |||   ||  | ||     |  |      |    |
Db    1084 GCCAAAGCCGGTTTGTTCTTGTGGATGGATTTAAGAAATCTTTTGAAGACAGCAACGTTT 1143

Qy     301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
           |    ||   ||| ||||||     | |  |  ||   |  ||| | |||||  ||||
Db    1144 GATTCGGAAACCGAACTATGGCGTGTGATTGTTCACCAAGTGAAGCTCAACGTGTCTCCA 1203

Qy     361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
           ||   ||  |  |||||   |||||| || |  |||||  | ||
Db    1204 GGCGGTTCGTTCCATTGCCATGAACCGGGATGGTTTAGAGTATG 1247


RESULT 5
US-10-114-170-72/c
; Sequence 72, Application US/10114170
; Publication No. US20030023075A1
;   GENERAL INFORMATION:
;        APPLICANT: Blattner, Frederick R.
;                   Burland,     Valerie
;                   Perna,  Nicole T.
;                   Plunkett, Guy
;                   Welch,  Rod
;        TITLE OF INVENTION: No. US20030023075A1el Sequences of E. coli O157
;        NUMBER OF SEQUENCES: 265
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Quarles & Brady
;             STREET: 1 South Pinckney Street
;             CITY: Madison
;             STATE: WI
;             COUNTRY: US
;             ZIP: 53701-2113
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Word Perfect 8.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/114,170
;             FILING DATE: 01-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/453,702
;             FILING DATE: 03-DEC-1999
;             APPLICATION NUMBER: 60/110,955
;             FILING DATE: 04-DEC-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Seay, Nicholas J.
;             REGISTRATION NUMBER: 27386
;             REFERENCE/DOCKET NUMBER: 960296.95017
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (608) 251-5000
;             TELEFAX: (608) 251-9166
;   INFORMATION FOR SEQ ID NO: 72:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 46819
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA  (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-114-170-72

  Query Match             7.8%;  Score 31.6;  DB 9;  Length 46819;
  Best Local Similarity   50.7%;  Pred. No. 6.4;
  Matches   76;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy     198 CGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
           | | | || |||  | | || |  ||    |||  ||  |||||  | || |||  ||
Db   37493 CATCGTGGCGGTGCAGGTAATTTCGCTGAAGATCGACAAAAAGCTTCTGACGCTGGTCGT 37434

Qy     258 TTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCT 317
               |||| ||||    |   | |||  |      | | | ||||   | |   |||
Db   37433 AAAGGCGGCCAACATAGTGGCGGTAATTTTAAAAACGATCCACAAAGAGCATCAGAAGCA 37374

Qy     318 ATGGGACAAGTTGCTAAACATTGCTAAGGT 347
           |  | ||| || | |  || || | |||
Db   37373 GGGAAAAAAGGTGGTCAGAATAGCCATGGT 37344


RESULT 6
US-09-938-842A-583
; Sequence 583, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
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;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 583
;   LENGTH: 1416
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-583

  Query Match             7.5%;  Score 30.4;  DB 9;  Length 1416;
  Best Local Similarity   57.3%;  Pred. No. 2.8;
  Matches   55;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy     300 AAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCC 359
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Db     306 AAAAACCGTTCTCATGCTTGCGGACCAGCTGATTAACAGAGTCGAGTTTATGCATACTAG 365

Qy     360 CGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTT 395
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Db     366 AGGTTTTCTTCACCGTGATATTAAACCTGACAACTT 401


RESULT 7
US-09-920-300A-1711/c
; Sequence 1711, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1711
;   LENGTH: 2302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1711

  Query Match             7.5%;  Score 30.2;  DB 10;  Length 2302;
  Best Local Similarity   51.1%;  Pred. No. 4.2;
  Matches   71;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy     145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
           |||||    | | |     |||||| |     ||  |||| |     ||| |||  | |
Db    2129 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 2070

Qy     205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGG 264
           |||| ||| ||  || |   ||  || |   |||   |||  | | ||||| |  |  |
Db    2069 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCAGGGCAGA 2010

Qy     265 GCCGACATGAGCGGATTGA 283
           |  |       |  || |||
Db    2009 GAGGCTGGCTGGAGAATGA 1991


RESULT 8
US-10-033-528-1711/c
; Sequence 1711, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  2001-12-26
;  NUMBER OF SEQ ID NOS: 1896
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1711
;   LENGTH: 2302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1711

  Query Match             7.5%;  Score 30.2;  DB 12;  Length 2302;
  Best Local Similarity   51.1%;  Pred. No. 4.2;
  Matches   71;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy     145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
           |||||    | | |     |||||| |     ||  |||| |     ||| |||  | |
Db    2129 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 2070

Qy     205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGG 264
           |||| ||| ||  || |   ||  || |   |||   |||  | | ||||| |  |  |
Db    2069 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCAGGGCAGA 2010

Qy     265 GCCGACATGAGCGGATTGA 283
           |  |       |  || |||
Db    2009 GAGGCTGGCTGGAGAATGA 1991


RESULT 9
US-09-764-869-2327/c
; Sequence 2327, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC007
;  CURRENT APPLICATION NUMBER: US/09/764,869
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2442
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
;   LENGTH: 7960
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-869-2327

  Query Match             7.5%;  Score 30.2;  DB 10;  Length 7960;
  Best Local Similarity   51.1%;  Pred. No. 7.9;
  Matches   71;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy     145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
           |||||    | | |     |||||| |     ||  |||| |     ||| |||  | |
Db    7780 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 7721

Qy     205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGG 264
           |||| ||| ||  || |   ||  || |   |||   |||  | | ||||| |  |  |
Db    7720 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCAGGGCAGA 7661

Qy     265 GCCGACATGAGCGGATTGA 283
           |  |       |  || |||
Db    7660 GAGGCTGGCTGGAGAATGA 7642


RESULT 10
US-09-764-869-2326/c
; Sequence 2326, Application US/09764869
; Patent No. US20020061521A1
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; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC007
;  CURRENT APPLICATION NUMBER: US/09/764,869
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2442
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
;   LENGTH: 17239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-869-2326

  Query Match             7.5%;  Score 30.2;  DB 10;  Length 17239;
  Best Local Similarity   51.1%;  Pred. No. 12;
  Matches   71;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
          |||||    | | |     ||||||  |     ||  |||| |     ||| |||  | |
Db  17059 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 17000

Qy    205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGG 264
          |||| ||| ||  || |   ||  || |   |||  ||| | | ||||| |  |  |
Db  16999 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCAGGGCAGA 16940

Qy    265 GCCGACATGAGCGGATTGA 283
          |  |      |  || |||
Db  16939 GAGGCTGGCTGGAGAATGA 16921


RESULT 11
US-09-924-035A-68
; Sequence 68, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
;  APPLICANT: Grlach, Jrn
;  TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;  TITLE OF INVENTION:  thaliana
;  FILE REFERENCE: 2011US
;  CURRENT APPLICATION NUMBER: US/09/924,035A
;  CURRENT FILING DATE:  2000-08-11
;  PRIOR APPLICATION NUMBER: US 60/148,784
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 900
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 353
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(353)
;   OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-68

  Query Match             7.4%;  Score 30;  DB 10;  Length 353;
  Best Local Similarity   53.1%;  Pred. No. 1.9;
  Matches   60;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy    288 ATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGT 347
          |||  |||  | ||||  | ||  | ||  || | |  || ||  |  |   | | ||
Db    135 ATCAGACAAAGCAAAACAAAAGGACAAGTAATAGAAGGAGCTGAAATCCTAAGGTTAGTG 194

Qy    348 AAACGTTACTCCCGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCC 400
          |||  ||| | ||||||  | | ||   || | ||||       |  ||  ||
Db    195 AAATTTTATTACCGGTTTCTTTCGTATCTGAAATGAAAANNNTCAACTTGTCC 247


RESULT 12
US-09-954-531-90
; Sequence 90, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
;  APPLICANT: Weaver, Zoe
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-77
;  CURRENT APPLICATION NUMBER: US/09/954,531
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: US/60/233,133
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,009
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,034
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,509
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US/60/234,567
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-90

  Query Match             7.4%;  Score 29.8;  DB 9;  Length 398;
  Best Local Similarity   54.0%;  Pred. No. 2.3;
  Matches   61;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
          |||||    | | |     ||||||  |     ||  |||| |     ||| |||  | |
Db    181 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 240

Qy    205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
          ||||  |||  ||  ||  |   ||  ||  |   |||   |||  | | |||||  |
Db    241 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCA 293


RESULT 13
US-09-954-531-291
; Sequence 291, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
;  APPLICANT: Weaver, Zoe
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-77
;  CURRENT APPLICATION NUMBER: US/09/954,531
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: US/60/233,133
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,009
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,034
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,509
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US/60/234,567
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 291
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-291

  Query Match             7.4%;  Score 29.8;  DB 9;  Length 398;
  Best Local Similarity   54.0%;  Pred. No. 2.3;
  Matches   61;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
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          |||||    | | |     ||||||  |     ||  ||||  |     ||| |||  | |
Db    181 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 240

Qy    205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
          ||||  ||| ||  ||  |   ||  ||  |   |||   |||  | | ||||| |
Db    241 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCA 293


RESULT 14
US-09-954-531-508
; Sequence 508, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
;  APPLICANT: Weaver, Zoe
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-77
;  CURRENT APPLICATION NUMBER: US/09/954,531
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: US/60/233,133
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,009
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,034
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,509
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US/60/234,567
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 508
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-508

  Query Match             7.4%;  Score 29.8;  DB 9;  Length 398;
  Best Local Similarity   54.0%;  Pred. No. 2.3;
  Matches   61;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
          |||||    | | |     ||||||  |     ||  ||||  |     ||| |||  | |
Db    181 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 240

Qy    205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
          ||||  ||| ||  ||  |   ||  ||  |   |||   |||  | | ||||| |
Db    241 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCA 293


RESULT 15
US-09-962-436-152
; Sequence 152, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
;  APPLICANT: Soppet, Daniel
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-75
;  CURRENT APPLICATION NUMBER: US/09/962,436
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,082
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/234,924
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 568
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 152
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-962-436-152

  Query Match             7.4%;  Score 29.8;  DB 10;  Length 398;
  Best Local Similarity   54.0%;  Pred. No. 2.3;
  Matches   61;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
          |||||    | | |     ||||||  |     ||  ||||  |     ||| |||  | |
Db    181 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 240

Qy    205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
          ||||  ||| ||  ||  |   ||  ||  |   |||   |||  | | ||||| |
Db    241 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCA 293


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